



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 166066

TO: Patricia Duffy
Location: rem/3B05/3C18
Art Unit: 1645
Wednesday, September 21, 2005

Case Serial Number: 09/647309

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Duffy,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524



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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 20, 2005, 21:28:53 ; Search time 41 Seconds
(without alignments)
807.282 Million cell updates/sec

Title: US-09-647-309A-2

Perfect score: 1822
Sequence: 1 MKALFVLNAPKNTWYAGG.....DRRVEIEVKGKVVETQPOA 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1781	97.7	356	2 JC6558	outer membrane pro
2	1551	85.1	350	2 S07222	outer membrane pro
3	1534.5	84.2	351	1 MNEBAD	outer membrane pro
4	1520	83.4	346	1 MNECA	outer membrane pro
5	1520	83.4	346	2 A90759	outer membrane pro
6	1520	83.4	346	2 G85622	outer membrane pro
7	1508	82.8	350	2 A10626	outer membrane pro
8	1499	82.3	350	1 MNEBAT	outer membrane pro
9	1381.5	75.8	359	2 S07298	outer membrane pro
10	1334.5	73.2	353	2 A00175	probable outer mem
11	1128.5	61.9	238	2 I62385	outer membrane pro
12	1112.5	61.1	244	2 I62393	outer membrane pro
13	1111	61.0	243	2 I62388	outer membrane pro
14	1110.5	60.9	242	2 I62389	outer membrane pro
15	1109	60.9	243	2 I84531	outer membrane pro
16	1106	60.7	243	2 I62386	outer membrane pro
17	1089	59.8	241	2 I62387	outer membrane pro
18	1084	59.5	241	2 I62391	outer membrane pro
19	1074.5	59.0	240	2 I62394	outer membrane pro
20	1056.5	58.0	238	2 I40703	outer membrane pro
21	646.5	35.5	353	2 C64187	outer membrane pro
22	515	28.3	349	2 E84968	outer membrane pro
23	443.5	24.3	321	2 F82104	outer membrane pro
24	271	14.9	194	2 A45275	21K outer membrane
25	262	14.4	236	2 A27894	outer membrane pro
26	255	14.0	242	2 C81205	outer membrane pro
27	251	13.8	240	2 A37004	outer membrane cla
28	250	13.7	242	2 A81782	outer membrane pro
29	243	13.3	326	2 S20494	root adhesin - Pse

outer membrane pro
OmpA family protei
outer membrane fib
outer membrane pro
outer membrane pro
probable outer mem
OmpA family protei
hypothetical 22.2K
probable outer mem
probable outer mem
probable outer mem
probable outer mem
hypothetical prote
probable ompA prot
probable membrane
probable lipoprote
conserved hypotet
peptidoglycan asso
probable outer mem
outer membrane pro
probable outer mem
probable outer mem
probable lipoprote
chemotaxis motB pr
flagellar motor pr
hypothetical prote
probable outer mem
probable lipoprote
OmpA family protei
porin [imported] -
peptidoglycan asso
peptidoglycan asso
outer membrane pro
OmpA family protei
pall protein - Pse
probable OmpA fami
outer membrane pro
probable outer mem
probable OmpA-fam
probable exported
hypothetical prote
hypothetical 17.2K
probable outer mem
probable outer mem
outer membrane pro
protein F-related
outer membrane pro
probable membrane
peptidoglycan-asso
omp16 protein - Br
motB protein homol
probable outer mem
omp16 protein [imp
omp16 protein [imp
peptidoglycan-asso
hypothetical prote
outer membrane pro
outer membrane pro
25K outer-membrane
31K outer-membrane
25K outer-membrane
extracellular prot
probable membrane
peptidoglycan-asso
31K outer-membrane
hypothetical prote
peptidoglycan-asso
probable outer mem
motility protein (oligo-1,6-glucosid
hypothetical prote
22K outer membrane

103 106.5 5.8 218 2 A82716 outer membrane pro
 104 106 5.8 28 2 A60752 outer membrane pro
 105 106 5.8 1343 2 E30893 hypothetical prote
 106 106 5.8 1343 2 D85724 hypothetical prote
 107 105.5 5.8 155 2 D71637 peptidoglycan-asso
 108 105.5 5.8 173 1 LPECPG peptidoglycan-asso
 109 105.5 5.8 173 2 H90725 peptidoglycan-asso
 110 105.5 5.8 173 2 A85577 peptidoglycan-asso
 111 105 5.8 275 2 A81160 motility protein (h
 112 104.5 5.7 230 2 A81480 25K outer-membrane
 113 104 5.7 317 2 F81407 probable periplasm
 114 103.5 5.7 155 2 H97849 peptidoglycan-asso
 115 103.5 5.7 247 2 D81453 probable flagellar
 116 103 5.7 281 2 A83012 outer surface prot
 117 103 5.7 284 2 G38271 hypothetical prote
 118 103 5.7 1325 2 A64905 ydeK protein - Esc
 119 102.5 5.6 188 2 C87649 OmpA family protei
 120 102.5 5.6 242 2 S39642 motility protein h
 121 101.5 5.6 211 2 S47347 outer membrane pro
 122 101 5.5 463 2 A83073 probable outer mem
 123 100.5 5.5 354 2 D75460 MoxR-related prote
 124 100 5.5 296 2 T46617 probable chemotaxi
 125 100 5.5 367 1 MMECPG outer membrane por
 126 99.5 5.5 1160 2 S32647 parasporal crystal
 127 99 5.4 176 2 A60337 outer membrane pro
 128 99 5.4 951 2 D75377 probable proteinase
 129 99 5.4 2554 2 A83528 extracellular seri
 130 98.5 5.4 188 2 E71495 probable peptidogl
 131 98.5 5.4 413 2 E70661 probable PE protei
 132 98.5 5.4 663 1 QREIC colicin I receptor
 133 98.5 5.4 866 1 C64834 probable outer mem
 134 98.5 5.4 1034 2 JC5569 serine proteinase
 135 98.5 5.4 1036 2 JC5568 serine proteinase
 136 98 5.4 160 2 H82207 hypothetical prote
 137 97.5 5.4 236 2 A13377 25K outer-membrane
 138 97.5 5.4 294 2 B82254 sodium-type flagel
 139 97.5 5.4 609 2 T42073 probable chitinase
 140 97.5 5.4 1218 2 J50069 hypothetical Pl op
 141 97 5.3 192 2 C86588 peptidoglycan-asso
 142 97 5.3 192 2 H72036 peptidoglycan-asso
 143 97 5.3 476 2 A71302 conserved hypotet
 144 96.5 5.3 254 2 F97127 flagellar motor pr
 145 96.5 5.3 391 2 A13375 rare lipoprotein A
 146 96.5 5.3 417 2 A91056 serine hydroxymeth
 147 96.5 5.3 417 2 E85900 serine hydroxymeth
 148 96.5 5.3 452 2 A60177 lambda maltoporin pr
 149 96.5 5.3 672 2 I40333 tracheal colonizat
 150 96 5.3 417 1 B48427 glycine hydroxymet
 151 96 5.3 513 1 A35742 aqualysin (EC 3.4.
 152 95.5 5.2 510 2 A81182 oligo-1,6-glucosid
 153 95.5 5.2 730 2 S70954 probable tape-meas
 154 95.5 5.2 1787 2 A81360 probable peptidogly
 155 95 5.2 174 2 A10592 peptidoglycan-asso
 156 95 5.2 250 2 G84054 hypothetical prote
 157 95 5.2 367 2 B85861 outer membrane pro
 158 95 5.2 367 2 H91016 outer membrane pro
 159 95 5.2 429 2 C83025 probable phosphose
 160 95 5.2 542 2 T29707 hypothetical prote
 161 95 5.2 873 1 S25193 outer membrane ush
 162 94.5 5.2 536 2 A10063 probable OmpA-fami
 163 94.5 5.2 1332 2 F69732 PBX prophage ORF
 164 94 5.2 261 2 B42882 motility protein (h
 165 94 5.2 417 1 XVECS glycine hydroxymet
 166 94 5.2 687 1 XUVKG UDPglucose 4-epime
 167 94 5.2 846 2 A82672 conserved hypotet
 168 94 5.2 848 2 B97454 hypothetical prote
 169 94 5.2 1165 2 S11446 parasporal crystal
 170 94 5.2 2399 2 H71879 toxin-like outer m
 171 93.5 5.1 202 2 G81653 peptidoglycan asso
 172 93.5 5.1 213 2 A56152 major 25K outer me
 173 93.5 5.1 274 2 AC3295 heat resistant agg
 174 93.5 5.1 364 2 D75539 branched-chain ami
 175 93.5 5.1 659 2 A85854 hypothetical prote

176 93.5 5.1 659 2 G91009 colicin I receptor
 177 93.5 5.1 3172 2 S22012 erythronolide synt
 178 93 5.1 278 2 D70504 hypothetical prote
 179 93 5.1 417 2 A80826 glycine hydroxymet
 180 93 5.1 445 2 E82075 hypothetical prote
 181 93 5.1 501 2 A13088 porin [imported] -
 182 93 5.1 506 2 A98198 hypothetical prote
 183 93 5.1 1010 2 I40329 brkA prtoein - Bor
 184 93 5.1 1829 2 A81864 hypothetical prote
 185 92.5 5.1 213 2 AC3408 25K outer-membrane
 186 92.5 5.1 301 2 S73387 hypothetical prote
 187 92.5 5.1 687 2 AG0495 alpha-amylase (EC
 188 92.5 5.1 730 2 T44313 hypothetical prote
 189 92.5 5.1 3163 2 A80233 yersiniabactin bio
 190 92.5 5.1 3163 2 T17440 probable polyketid
 191 92 5.0 788 2 C82595 ferric enterobacti
 192 92 5.0 880 2 AF2128 hypothetical prote
 193 92 5.0 1061 2 A40609 OmpA-related prote
 194 91.5 5.0 389 2 G70120 outer membrane pro
 195 91.5 5.0 463 2 T10015 hypothetical prote
 196 91.5 5.0 488 2 F86911 conserved hypotet
 197 91.5 5.0 1238 2 A64596 hypothetical prote
 198 91.5 5.0 1291 2 S44983 vacuolating cyto
 199 91 5.0 350 2 S32878 hydrogenase expres
 200 91 5.0 590 2 E70946 probable PPE prote
 201 91 5.0 2204 2 A70524 probable PPE prote
 202 90.5 5.0 313 2 A80734 probable bacteriop
 203 90.5 5.0 447 2 E82729 outer membrane pro
 204 90.5 5.0 452 2 AF1014 maltoporin precurs
 205 90.5 5.0 666 2 F83340 hypothetical prote
 206 90.5 5.0 1286 2 S28634 adhesin AIDA-I pre
 207 90.5 5.0 3161 2 T30342 protein HMWp1 - Ye
 208 90 4.9 429 2 S23581 lambda protein precu
 209 90 4.9 562 2 A81335 probable peptidogl
 210 90 4.9 2109 2 T38414 transcription fact
 211 90 4.9 3434 1 G97VMV genome polyprotein
 212 90 4.9 3972 2 S75251 hypothetical prote
 213 89.5 4.9 781 2 T36143 probable secreted
 214 89.5 4.9 819 2 B87580 conserved hypotet
 215 89.5 4.9 863 2 A80525 outer membrane ush
 216 89.5 4.9 971 2 C75503 hypothetical prote
 217 89 4.9 207 2 AF0199 probable lipoprote
 218 89 4.9 625 2 AD0476 probable vitamin B
 219 89 4.9 669 2 B96036 probable aldehyde
 220 89 4.9 754 2 AC2807 OmpA family protei
 221 89 4.9 754 2 B97586 hypothetical prote
 222 89 4.9 775 2 T00962 hypothetical prote
 223 89 4.9 1651 2 JC1340 outer membrane pro
 224 89 4.9 5627 2 C83339 hypothetical prote
 225 88.5 4.9 507 2 A55625 protein-tyrosine k
 226 88.5 4.9 692 2 A84963 amine oxidase (cop
 227 88.5 4.9 807 2 A38152 F-spondin - rat
 228 88 4.8 394 2 T46858 molybdenum cofacto
 229 88 4.8 484 2 B70586 probable amIA2 pro
 230 88 4.8 1068 2 E81965 probable outer mem
 231 88 4.8 1215 2 T11660 probable RNA-direc
 232 87.5 4.8 388 2 G95159 chorismate synthas
 233 87.5 4.8 388 2 G98025 chorismate synthas
 234 87.5 4.8 445 2 S73703 hypothetical prote
 235 87.5 4.8 479 1 S26699 alkaline metallopr
 236 87.5 4.8 664 2 A11237 transketolase homo
 237 87.5 4.8 794 2 T36972 probable membrane
 238 87.5 4.8 832 2 G85497 probable fibrial
 239 87.5 4.8 836 2 D64988 yefJ protein - Esc
 240 87.5 4.8 866 2 G90646 TonB-dependent rec
 241 87.5 4.8 1035 2 C87373 hypothetical prote
 242 87.5 4.8 1037 2 S51900 hypothetical prote
 243 87.5 4.8 1302 2 T00038 hypothetical prote
 244 87.5 4.8 1684 2 JW0057 gravin - human
 245 87.5 4.8 3300 2 D70575 probable PPE prote
 246 87.5 4.8 3716 2 E70969 probable PPE prote
 247 87 4.8 256 2 C96937 chemotaxis motilit
 248 87 4.8 428 2 A87540 histidinol dehydro

249 87 4.8 442 2 G84778 probable bZIP tran
250 87 4.8 467 2 F64765 yaiU protein - Bsc
251 87 4.8 682 2 C84295 UDP-sugar hydrolas
252 87 4.8 980 2 H30681 probable flagellin
253 87 4.8 980 2 D85532 probable structure
254 86.5 4.7 350 2 E82181 aldose 1-epimerase
255 86.5 4.7 371 2 A10147 outer membrane pro
256 86.5 4.7 571 2 S61889 3-oxosteroid 1-deh
257 86.5 4.7 537 2 A35400 surface protein T6
258 86.5 4.7 638 2 AH0340 putative autotransp
259 86.5 4.7 752 2 AG0782 colicin I receptor
260 86.5 4.7 752 2 T06838 probable photosyst
261 86.5 4.7 1108 1 S45917 probable serine/th
262 86.5 4.7 1404 2 E85509 hypohetical prote
263 86.5 4.7 1404 2 E90658 RhaG core protein
264 86 4.7 222 2 E71644 hypohetical prote
265 86 4.7 239 2 AH0541 probable outer mem
266 86 4.7 377 2 D64888 outer membrane por
267 86 4.7 423 2 A84483 probable protein k
268 86 4.7 444 2 E96584 hypohetical prote
269 86 4.7 493 2 S73752 hypohetical prote
270 86 4.7 572 2 S77249 hypohetical prote
271 86 4.7 608 2 H75089 twitching mobility
272 86 4.7 877 2 JN0772 glucan endo-1,3-be
273 86 4.7 890 2 T35237 probable secreted
274 86 4.7 1052 2 H83909 cell wall-associat
275 86 4.7 1374 2 A83259 extracellular seri
276 86 4.7 1417 2 H90670 probable adhesin l
277 86 4.7 201 2 D85521 probable adhesin e
278 85.5 4.7 201 2 A75506 hypohetical prote
279 85.5 4.7 613 2 S50721 dnaK-type molecula
280 85.5 4.7 698 2 D90771 hypohetical prote
281 85.5 4.7 698 2 H85633 hypohetical prote
282 85.5 4.7 698 2 F64839 yegH protein precu
283 85.5 4.7 888 2 F87500 hypohetical prote
284 85.5 4.7 1008 2 G82732 hypohetical prote
285 85.5 4.7 1097 2 T31504 hypohetical prote
286 85 4.7 351 2 A38528 outer membrane por
287 85 4.7 378 1 M8EBPC outer membrane por
288 85 4.7 378 2 A10789 outer membrane pro
289 85 4.7 511 2 D97965 hypohetical prote
290 85 4.7 511 2 H95097 sugar ABC transpor
291 85 4.7 529 1 M2EC8 58K mobilization p
292 85 4.7 630 2 S77346 hypohetical prote
293 85 4.7 801 2 T07617 proteinase TMP - t
294 85 4.7 829 2 AG0869 probable outer mem
295 85 4.7 874 2 E75278 hypohetical prote
296 85 4.7 1289 2 A82217 hypohetical prote
297 84.5 4.6 263 2 E69445 conserved hypotet
298 84.5 4.6 278 1 I40838 2,5-diketo-D-gluc
299 84.5 4.6 409 2 F90645 hypohetical prote
300 84.5 4.6 409 2 F85496 hypohetical prote

ALIGNMENTS

RESULT 1
JC6558
outer membrane protein A precursor - Klebsiella pneumoniae
C;Species: Klebsiella pneumoniae
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
C;Accession: JC6558
R;Nguyen, T.N.; Samuelson, P.; Sterky, F.; Merle-Poitte, C.; Robert, A.; Bauseant, T.; H
Gene 210, 93-101, 1998
A;Title: Chromosomal sequencing using a PCR-based biotin-capture method allowed isolatic
A;Reference number: JC6558; MUID:98192544; PMID:9524233
A;Accession: JC6558
A;Molecule type: DNA
A;Residues: 1-356 <NGU>
A;Experimental source: IP I145
C;Genetics:
A;Gene: ompA

C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-356/Product: outer membrane protein A #status predicted <MAT>
Query Match 97.7%; Score 1781; DB 2; Length 356;
Best Local Similarity 99.1%; Pred. No. 3.9e-127;
Matches 336; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Oy 6 VLNAAPKDNWTYAGGKLGWSQYHDTGFYNGFNQNNGPTNRNDQLGAGAFGGYQVNPYLG 65
Db 18 VAQAAPKDNWTYAGGKLGWSQYHDTGFYNGFNQNNGPTNRNDQLGAGAFGGYQVNPYLG 77
Oy 66 EMGYDWLGRMAYKGSVDNGAFKAGQVLTAKLGYPIITDDLDIYTRLGGMWWRADSKGNYA 125
Db 78 EMGYDWLGRMAYKGSVDNGAFKAGQVLTAKLGYPIITDDLDIYTRLGGMWWRADSKGNYA 137
Oy 126 STGVSRSRSHDTGVSVPFAGGVWAVTRDIATRLRYQVWNNIGDAGTGTGTRPDNGMLSGV 185
Db 138 STGVSRSRSHDTGVSVPFAGGVWAVTRDIATRLRYQVWNNIGDAGTGTGTRPDNGMLSGV 197
Oy 186 SYRFGQEDAAPVAP 245
Db 198 SYRFGQEDAAPVAP 257
Oy 246 MDPKDGSAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
Db 258 MDPKDGSAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 317
Oy 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGVEVVTQPA 344
Db 318 GNTCDNVKARAALIDCLAPDRRVEIEVKGVEVVTQPA 356
RESULT 2
S07222
outer membrane protein ompA precursor - Enterobacter aerogenes
C;Species: Enterobacter aerogenes
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: S07222
R;Braun, G.; Cole, S.T.
Eur. J. Biochem. 137, 495-500, 1983
A;Title: Molecular characterization of the gene coding for major outer membrane protein
A;Reference number: S07222; MUID:84108348; PMID:6363059
A;Accession: S07222
A;Molecule type: DNA
A;Residues: 1-350 <BRA>
A;Cross-references: UNIPROT:P09146; EMBL:X00254; NID:G40837; PIDN:CAA2S062.1; PID:G40838
A;Note: the authors translated the codon CAG for residue 197 as Asn
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-350/Product: outer membrane protein ompA #status predicted <MAT>
F;201-212/Region: alanine/proline-rich
F;213-350/Domain: periplasmic #status predicted <PER>

Query Match 85.1%; Score 1551; DB 2; Length 350;
Best Local Similarity 87.6%; Pred. No. 9.2e-110;
Matches 297; Conservative 10; Mismatches 26; Indels 6; Gaps 2;
Oy 6 VLNAAPKDNWTYAGGKLGWSQYHDTGFYNGFNQNNGPTNRNDQLGAGAFGGYQVNPYLG 65
Db 18 VAQAAPKDNWTYAGGKLGWSQYHDTGFYNGFNQNNGPTNRNDQLGAGAFGGYQVNPYLG 76
Oy 66 EMGYDWLGRMAYKGSVDNGAFKAGQVLTAKLGYPIITDDLDIYTRLGGMWWRADSKGNYA 125
Db 77 EMGYDWLGRMPYKGVKNVAFSSQAVLTAKLGYPIITDDLDIYTRLGGMWWRADSKGNYA 131
Oy 126 STGVSRSRSHDTGVSVPFAGGVWAVTRDIATRLRYQVWNNIGDAGTGTGTRPDNGMLSGV 185
Db 132 SNSIAGDNHDTGVSVPFAGGVWAVTRDIATRLRYQVWNNIGDAGTGTGTRPDNGMLSGV 191

Db 18 VAQAAPKDNWTWYAGAKLGWSQYHDTGFI-----HNDGPTHEYNQLGAGAFGGYQVNPYVG 72

Qy 66 EMGYDNLGRMAYKGSVDNGAFKAQGVQLTAKLGYPIITDDLDIYTRFLGGMWRADSKGNYA 125

Db 73 EMGYDNLGRMPYKGDNTNGAYKAQGVQLTAKLGYPIITDDLDIYTRFLGGMWRADTKSNVP 132

Qy 126 STGVSRSSEHDTGVSVPFAGGVEMAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185

Db 133 G-GASTKDHDTGVSVPFAGGIEYAITPEIATRLLEYQWVNNIGDANTIGTRPDNGLLSVGV 191

Qy 186 SYRFQGEADAAPVAPAPAPAEVATKHTFLKSDVLFNFNKATLKPGEQQALDQLYTQLSN 245

Db 192 SYRFQGEAAAPVAPAPAPAEVQTKHTFLKSDVLFNFNKSTLKPGEQQALDQLYSQLSN 251

Qy 246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305

Db 252 LDPKDGSSVVVLGFTDRIGSDAYNQQLSEKRAQSVVDYLISKGIPSDKISARGMGESNPVT 311

Qy 306 GNTCDNVKRAALIDCLAPDRRVEIEVKGYKEVVTPQQA 344

Db 312 GNTCDNVKPRALIDCLAPDRRVEIEVKGVKDVVTQQA 350

RESULT 8

MMEBAT

outer membrane protein A precursor - Salmonella typhimurium

N:Alternate names: outer membrane major heat-modifiable protein; outer membrane protein

C:Species: Salmonella typhimurium

C>Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004

C:Accession: A03436

R:Freudl, R.; Cole, S.T.

Eur. J. Biochem. 134, 497-502, 1983

A:Title: Cloning and molecular characterization of the ompA gene from Salmonella typhimurium

A:Reference number: A03436; MUID:83287368; PMID:6349993

A:Accession: A03436

A:Molecule type: DNA

A:Residues: 1-350 <FRE>

A:Cross-references: UNIPROT:P02936; GB:X02006; NID:g47798; PIDN:CAA26037.1; PID:g758341

C:Genetics:

A:Gene: ompA

A:Map position: 20 min

C:Function:

A:Description: required for the action of colicins and for the stabilization of mating a

A>Note: cannot serve as the receptor for the ompA-specific phages K3 and TuII

C:Superfamily: outer membrane protein A

C:Keywords: transmembrane protein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-350/Product: outer membrane protein A #status predicted <MAT>

F:22-200/Domain: intramembrane #status predicted <INT>

F:200-212/Region: alanine/proline-rich

F:213-350/Domain: periplasmic #status predicted <PER>

Query Match 82.3%; Score 1499; DB 1; Length 350;

Best Local Similarity 82.9%; Pred. No. 7.8e-106;

Matches 281; Conservative 24; Mismatches 28; Indels 6; Gaps 2;

Qy 6 VLNAAPKDNWTWYAGKLGWSQYHDTGFI-----HNDGPTHEYNQLGAGAFGGYQVNPYLG 65

Db 18 VAQAAPKDNWTWYAGAKLGWSQYHDTGFI-----HNDGPTHEYNQLGAGAFGGYQVNPYVG 72

Qy 66 EMGYDNLGRMAYKGSVDNGAFKAQGVQLTAKLGYPIITDDLDIYTRFLGGMWRADSKGNYA 125

Db 73 EMGYDNLGRMPYKGDNTNGAYKAQGVQLTAKLGYPIITDDLDIYTRFLGGMWRADTKSNVP 132

Qy 126 STGVSRSSEHDTGVSVPFAGGVEMAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185

Db 133 G-GPSTKDHDTGVSVPFAGGIEYAITPEIATRLLEYQWVNNIGDANTIGTRPDNGLLSVGV 191

Qy 186 SYRFQGEADAAPVAPAPAPAEVATKHTFLKSDVLFNFNKATLKPGEQQALDQLYTQLSN 245

Db 192 SYRFQGEAAAPVAPAPAPAEVQTKHTFLKSDVLFNFNKSTLKPGEQQALDQLYIQLSN 251

Qy 246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305

Db 252 LDPKDGSSVVVLGFTDRIGSDAYNQQLSEKRAQSVVDYLISKGIPSDKISARGMGESNPVT 311

Qy 306 GNTCDNVKRAALIDCLAPDRRVEIEVKGYKEVVTPQQA 344

Db 312 GNTCDNVKPRALIDCLAPDRRVEIEVKGVKDVVTQQA 350

RESULT 9

S07298

outer membrane protein ompA precursor - Serratia marcescens

C:Species: Serratia marcescens

C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004

C:Accession: S07298

R:Braun, G.; Cole, S.T.

Mol. Gen. Genet. 195, 321-328, 1984

A:Title: DNA sequence analysis of the Serratia marcescens ompA gene: implications for th

A:Reference number: S07298; MUID:85035845; PMID:6092858

A:Accession: S07298

A:Molecule type: DNA

A:Residues: 1-359 <BRA>

A:Cross-references: UNIPROT:P04845; EMBL:X00618; NID:g47242; PIDN:CAA25254.1; PID:g758303

C:Genetics:

A:Gene: ompA

C:Superfamily: outer membrane protein A

C:Keywords: membrane protein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-359/Product: outer membrane protein ompA #status predicted <MAT>

F:22-209/Domain: intramembrane #status predicted <INT>

F:210-219/Region: alanine/proline-rich

F:220-359/Domain: periplasmic #status predicted <PER>

Query Match 75.8%; Score 1381.5; DB 2; Length 359;

Best Local Similarity 78.4%; Pred. No. 6.2e-97;

Matches 269; Conservative 24; Mismatches 43; Indels 7; Gaps 4;

Qy 6 VLNAAPKDNWTWYAGKLGWSQYHDTGFI-----HNDGPTHEYNQLGAGAFGGYQVNPYL 63

Db 18 VAQAAPKDNWTWYAGKLGWSQYHDTGFI-----HNDGPTHEYNQLGAGAFGGYQVNPYL 77

Qy 64 GFEMGYDNLGRMAYKGSVDNGAFKAQGVQLTAKLGYPIITDDLDIYTRFLGGMWRADSKGN 123

Db 78 GFELGYDNLGRMPYKGSVNNNGAFKAQGVQLAALKSYPIADDDLDIYTRFLGGMWRADSKAN 137

Qy 124 YASTGVSRSSEHDTGVSVPFAGGVEMAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSL 183

Db 138 YGRTGQRLSDHDTGVSFLAAVGVVEYALTKNWATRLDYQFVSNIGDAGTVGARPNTMLSL 197

Qy 184 GVSYRFGQED-AAAPVAPAPAPAEVATKHTFLKSDVLFNFNKATLKPGEQQALDQLYTQ 242

Db 198 GVSYRFGQDDVAP--APAPAPAPVETKRTFLKSDVLFNFNKSTLKAEGQALDQLYTQ 255

Qy 243 LSNMDDPKGSAAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESN 302

Db 256 LSSMDPKGSSVVVLGYTDAVGSQYQNLSEKRAQSVVDYLVSXGIPSDKISARGMGESN 315

Qy 303 PVTGNTCDNVKARA--ALIDCLAPDRRVEIEVKGYKEVVTPQ 343

Db 316 AVTGNTCGYKSGRATKAQIVCLAPDRRVEIEVKGIKDVVTQ 358

RESULT 10

AD0175

probable outer membrane porin A protein ompA [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C:Accession: AD0175

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AD0175
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-353 <KUR>
A:Cross-references: UNIPROT:Q8ZG77; GB:AL590842; PIDN:CAC90263.1; PID:g15979482; GSPDB:G
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A

Query Match 73.2%; Score 1334.5; DB 2; Length 353;
Best Local Similarity 75.4%; Pred. No. 2.2e-93;
Matches 257; Conservative 28; Mismatches 49; Indels 7; Gaps 4;

QY 6 VLNAAPKONTWYAGKLGHSQVHDTGFGYNGFQNNNGPTRNDQLGAGAFGGYQVNPYLG 65
DB 18 VAQAAPKONTWYTGKLGHSQVQDTG----SIINNDGPTHKDLGAGAFFGQYQANQYLG 73

QY 66 EMGYDMLGRMAYKGSVDNCAKQGVOLTKLGYPTDLDIYTRLGGMVWRADSKGNVA 125
DB 74 EMGYDMLGRMPYKGDINNGAFKAQGVQAAKLSYVAQDLDVYTRLGGLWRADAKGSF- 132

QY 126 STGVSR-SGSHDTGVSFPAGGVAVTRDIAATREYQWNNIGDAGTVGTRPDNGMLSIG 184
DB 133 DGLDRASGHDGVSPLVALGAYAWTKNATREYQWNNIGDRETVGARPDNGLLSVG 192

QY 185 VSYRFGQED-AAPVVAPAPAPAPAEVATKHTLTKSDVLFNFNFKATLKPEGQALDQLYTQL 243
DB 193 VSYRFGQEDAAPIVAPTAPAPAPIVDTKRFTLTKSDVLFNFNFKATLKPEGQALDQLYAQL 252

QY 244 SNMDPKGSANVLGYTDIGSFAYNQOLSEKRAQSVVDLYVAKGIPAGKISARGMGESNP 303
DB 253 SSIDPKGGSVVVLGFPADRIQGPAPNALSRADSVRYLVSKGIPADKITARGEGQANP 312

QY 304 VTGNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTOPOA 344
DB 313 VTGNTCDNVKPAALIECLAPDRRVEIEVKYKEVVTOPOA 353

RESULT 11
I62385
outer membrane protein ompA - Escherichia vulneris (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia vulneris
C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
A:Accession: I62385
J:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: 140701; PMID:92065252; PMID:1955870
A:Status: preliminary;
A:Cross-references: UNIPROT:Q99114; GB:M63348; PIDN:AAA24233.1; PID:g146985
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:98-109/Region: alanine/proline-rich

Query Match 61.9%; Score 1128.5; DB 2; Length 238;
Best Local Similarity 90.1%; Pred. No. 4.8e-78;
Matches 219; Conservative 7; Mismatches 12; Indels 5; Gaps 1;

QY 93 LTAKLGYPTDLDIYTRLGGMVWRADSKGNVASTGVSRSEHDTGVSVPFAGGVAVTR 152
DB 1 LTAKLGYPTDLDIYTRLGGMVWRADSKGNVASTGVSRSEHDTGVSVPFAGGVAVTR 55

QY 153 DIATREYQWNNIGDAGTVGTRPDNGMLSLGVSRFGQEDAAPVVAPAPAPAEVATK 212
DB 56 DIATREYQWNNIGDAGTVGTRPDNGMLSLGVSRFGQEDAAPVVAPAPAPAEVATK 115

QY 213 FTLKSDVLFNFNFKATLKPEGQALDQLYTQLSNMDPKGSVAVLGYTDRIGSEAYNQOLS 272

DB 116 FTLKSDVLFNFNFKATLKPEGQALDQLYTQLSNMDPKGSVAVLGYTDRIGSEAYNQOLS 175
QY 273 EKRAQSVVDLYVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 332
DB 176 EKRAQSVVDLYVAKGIPANKISARGMGESDPTGNTCDNVKARAALIDCLAPDRRVEIEV 235

QY 333 KGY 335
DB 236 KGY 238

RESULT 12
I62393
outer membrane protein ompA - Escherichia vulneris (ATCC 33822) (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia vulneris
A:Variety: ATCC 33822
C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: I62393
J:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: 140701; PMID:92065252; PMID:1955870
A:Accession: I62393
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-244 <RES>
A:Cross-references: UNIPROT:Q47880; GB:M63350; PIDN:AAA24241.1; PID:g147001
A:Experimental source: ATCC 33822
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:104-115/Region: alanine/proline-rich

Query Match 61.1%; Score 1112.5; DB 2; Length 244;
Best Local Similarity 87.2%; Pred. No. 8.1e-77;
Matches 212; Conservative 15; Mismatches 15; Indels 1; Gaps 1;

QY 93 LTAKLGYPTDLDIYTRLGGMVWRADSKGNVASTGVSRSEHDTGVSVPFAGGVAVTR 152
DB 1 LTAKLGYPTDLDIYTRLGGMVWRADAKAQVPTGASFKDHDGVSVPFAGGVAVTR 60

QY 153 DIATREYQWNNIGDAGTVGTRPDNGMLSLGVSRFGQEDAAPVVAPAPAPAEVATK 211
DB 61 DIATREYQWNNIGDAGTVGTRPDNGMLSLGVSRFGQEDAAPVVAPAPAPAEVATK 120

QY 212 HFTLKSDVLFNFNFKATLKPEGQALDQLYTQLSNMDPKGSVAVLGYTDRIGSEAYNQOL 271
DB 121 HFTLKSDVLFNFNFKATLKPEGQALDQLYTQLSNMDPKGSVAVLGYTDRIGSDAYNQOL 180

QY 272 SEKRAQSVVDLYVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIE 331
DB 181 SEKRAQSVVDLYLTKGIPSNKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIE 240

QY 332 VKG 334
DB 241 VKG 243

RESULT 13
I62388
outer membrane protein A - Escherichia fergusonii (ATCC 35472) (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia fergusonii
A:Variety: ATCC 35472
C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: I62388; I62392
J:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: 140701; PMID:92065252; PMID:1955870

Query Match	59.8%	Score 1089;	DB 2;	Length 241;
Best Local Similarity	86.0%	Pred. No. 4.7e-75;		
Matches 208;	Conservative	17;	Mismatches 15;	
			Indels	2;
			Gaps	1;

RESULT 22
E84968
outer membrane protein A precursor [imported] - Buchnera sp. (strain APS)
C:Species: Buchnera sp.
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 03-Jun-2002
C:Accession: E84968
R:Shigenobu, S.; Matanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A>Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: E84968
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: ompA; BU332
C:Superfamily: outer membrane protein A

Query Match 28.3%; Score 515; DB 2; Length 349;
Best Local Similarity 35.3%; Pred. No. 1.9e-31;
Matches 116; Conservative 60; Mismatches 141; Indels 12; Gaps 6;
QY 10 APKNTWTAGKLGWSQVHDGTFYNGNGFONNNGPTRNDOLGA---GAFGGYQVNPYLGFE 66
DB 22 AEEENGWYLGAKFGWGHFNPLKDYDMNSQVNNDSSENLSAPIVGLPLGYEFNPYFSL 81
QY 67 MGYDWLGRWAYK-GSVNDNGAFKAQGVLTAKLGYPTDLDIYTRLGGMV-WRADSKGNY 124
DB 82 IENDTNGFFPHLIFOKNNEHQSNVQLATKLSYPTDFEFLYTKLGIGVSNNDLSSKNT 141
QY 125 ASTGVSRSSEHDTGSPVPAGGVEMAVTRDIATRLFYQVWNNIGDAGTGTGTPDNGMLSLG 184
DB 142 LKNLFSK---ESALLPSLSLGAEIFNFTFTRLDYTWNSVKNIANASIKPALGDAVLS 198
QY 185 VSYRFGQEDAAPVAPAPA-PAPEVATKHTLKSDFLNFNFKATLKPEGQALDQLYTQL 243
DB 199 IGWFKGKSDISMFSDDSEPLNE---QYSLVNNENINFPNSTELKPSYDKLNKLDLDDI 255
QY 244 SNMDPKDSAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNP 303
DB 256 KDMQLKNVSIIVLLGHADKIGSDYXQKLSEDRAVSIKNYLASRFGFSRDKITVKGMGKLYP 315
QY 304 VTGNTCDNVKARAALIDCLAPDRRVEIEV 332
DB 316 LTNQCRDVNKNPLLSICLAPDRRVEIEV 344

RESULT 23
F82104
outer membrane protein OmpA VC2213 [imported] - Vibrio cholerae (strain N16961 serogroup
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: F82104
R:Heidelber, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P.
l. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: F82104
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-321 <HE1>
A:Cross-references: UNIPROT:O31154; GB:AE004293; GB:AE003852; NID:g9656766; PIDN:AAF9535
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2213
A:Map position: 1
C:Superfamily: outer membrane protein A

Query Match 24.3%; Score 443.5; DB 2; Length 321;
Best Local Similarity 36.3%; Pred. No. 4.3e-26;
Matches 122; Conservative 49; Mismatches 116; Indels 49; Gaps 12;
QY 17 YAGKLGWSQVHDGTFYNGNGFONNNGPTRNDOLCAGAFGGYQVNPYLGFEFGYDWLGRMA 76
DB 24 YVGKVKSWLDDACLAGQSCD-----DDQV-VGAFGLQYQANKWLSLEAGYDYLKFT 76
QY 77 YKGSVDNGAFKAQGVLTAKLGYPTDLDIYTRLGGMWRADSKGNYASTVSRSSEHDT 136
DB 77 AAGLNDE---KVQAVTLAPKLSIFLTREGIALYKVGAYVDYGSKDDYSYLG----- 125
QY 137 GVSVPFAGGVEMAVTRDIATRLFYQVWNNIGDAGTGTGTPDNGMLSLGVSYRF-GQEDAA 195
DB 126 -----AAGLEFNTNHNVTMRLEYQ---NLTDINDIVRAAEATATLGIAIKFGGSEBPA 176
QY 196 PVV-----APAPAPAEVA-TKHFTLK--SDVLEFNFKATLKPEGOALDQLYTQLSN 245
DB 177 PVQEORPAEPAPVAPVEKVAVTFTFQHLDSFTFATASAEALPAPATVKLDKIVGYL-N 235
QY 246 MDPKDSAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
DB 236 QYPQ-AKVEVVGHDTSTGSEAYNQKLSERRAQAQAKALEAQGIDASRISAKGLGESSPIA 294
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYSVVTO 341
DB 295 SN-----ATAEGREKNRRVELVPEFQYQVTE 321

RESULT 24
A45275
21k outer membrane protein OmpA - Bordetella avium
C:Species: Bordetella avium
C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A45275
R:Gentry-Weeks, C.R.; Hultsch, A.L.; Kelly, S.M.; Keith, J.M.; Curtiss III, R.
J. Bacteriol. 174, 7729-7742, 1992
A>Title: Cloning and sequencing of a gene encoding a 21-kilodalton outer membrane protein.
A:Reference number: A45275; MUID:93077456; PMID:1447140
A:Contents: 197
A:Accession: A45275
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-194 <GEN>
A:Cross-references: UNIPROT:Q05146; GB:M96550; NID:g144051; PIDN:AAA22979.1; PID:g144052
A>Note: sequence extracted from NCBI backbone (NCBI:P:119132)
C:Superfamily: outer membrane protein A

Query Match 14.9%; Score 271; DB 2; Length 194;
Best Local Similarity 36.5%; Pred. No. 2.4e-13;
Matches 76; Conservative 25; Mismatches 67; Indels 40; Gaps 7;
QY 141 VFAGGVEMAVTRDIATRLFYQVWNNIGDAGTGTGTR-----PDNGMLSLGVSYRFG 190
DB 16 VTASGVASQTVD-----NWRNPYGNVWKNNGNELCWRDADFWTPTATGPGC----- 61
QY 191 QEDAAPVY-APAPAPAEVATKHFTLKSDFLNFNFKATLKPEGOALDQLYTQLSNMDPK 249
DB 62 --DGVPAVQPKPEKAPMAAKVVF--NADTFDFDKSTLKEGRLQDQVAQQAIDLE 117
QY 250 DGSNAVLYGTYDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTC 309
DB 118 --TIIAVGNTDSIGTEAYNMKLSERRAASVAVLVSKGIDPNRIYTEGKGLNPIASNKT 175
QY 310 DNKARAALIDCLAPDRRVEIEVKGYSKE 337
DB 176 AEGRAR-----NRRVEIIVGSRK 194

RESULT 25
A27894
outer membrane protein PIII precursor - Neisseria gonorrhoeae
N:Alternate names: gonococcal protein III; PIII

C;Species: Neisseria gonorrhoeae
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A27894; A60817
R;Gotschlich, E.C.; Seiff, M.; Blake, M.S.
J. Exp. Med. 165, 471-482, 1987
A;Title: The DNA sequence of the structural gene of gonococcal protein III and the flank
A;Reference number: A27894; MUID:87139801; PMID:3102671
A;Accession: A27894
A;Molecule type: DNA
A;Residues: 1-236 <GOT>
A;Cross-references: UNIPROT:P07050; GB:X05105; NID:g44889; PIDN:CAA28752.1; PID:g44890
R;Gotschlich, E.C.; Blake, M.S.; Lytton, E.J.; Seiff, M.
Antonie Van Leeuwenhoek 53, 455-459, 1987
A;Title: Gonococcal protein III. Purification and chemical characterization of the prote
A;Reference number: A60817; MUID:86221126; PMID:3130783
A;Accession: A60817
A;Molecule type: protein
A;Residues: 23-30,'X',32 <GOS>
C;Keywords: membrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;22-236/Product: outer membrane protein PIII #status experimental <MAT>

Query Match 14.4%; Score 262; DB 2; Length 236;
Best Local Similarity 35.0%; Pred. No.1.5e-12;
Matches 69; Conservative 29; Mismatches 67; Indels 32; Gaps 6;

Qy 164 NNIGDA--GTGTRPDNGMLSLGVSYRFGQEDAAPVAPAP-----APEVATKHFTL 215
Db 42 NNYGECWKNAYFDKASQGRVCEG-----DAVAPPEPAPVAVVEQAPQYVDETISL 93

Qy 216 KSDVLFNFNFKATLKPEGOQALDQLYTOLSNMDPKDGSAAVLGYTDRIIGSEAYNQOLSEK 275
Db 94 SAKTLFGFDKSLRAEAQNLKVLQRLSRITVQ--SVRVEGHTDFMGSEKYNQALSERR 151

Qy 276 AQSVVDYLVAKGIPAGKISARGMESNPVTGNTC-----DNVKAALIDCLAP 324
Db 152 AVVANNLVNGVPASRISAVGLGESQAQMTQVCEAVKLGAKAKKAKREALIACIEP 211

Qy 325 DRRVEIEVKGYKEVVTQ 341
Db 212 DRRVDVKI---RSIVTR 225

RESULT 26
C81205
outer membrane protein class 4 NMB0382 [imported] - Neisseria meningitidis (strain MC58
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C81205
R;Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: C81205
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-242 <TET>
A;Cross-references: UNIPROT:P38367; GB:AE002394; GB:AE002098; NID:g7225599; PIDN:AAF4082
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0382

Query Match 14.0%; Score 255; DB 2; Length 242;
Best Local Similarity 33.3%; Pred. No. 5.3e-12;
Matches 65; Conservative 34; Mismatches 74; Indels 22; Gaps 5;

Qy 164 NNIGDA--GTGTRPDNGMLSLGVSYRFGQEDAAPVAPAP-----PAPEVATKHFTLS 217
Db 42 NNYGECWKNAYFDKASQGRVCEGDAVAAPEPEPEPAPVAVVEQAPQYVDETISLSA 101

218 DVLNFNFKATLKPEGOQALDQLYTOLSNMDPKDGSAAVLGYTDRIIGSEAYNQOLSEKRAQ 277
Db 102 KTLFGFDKSLRAEAQNLKVLQRLSRITVQ--SVRVEGHTDFMGSDKYNQALSERRAY 159

Qy 278 SVVDYLVAKGIPAGKISARGMESNPVTGNTC-----NVKARAALIDCLAPDR 326
Db 160 VVANNLVNGVPVSRISAVGLGESQAQMTQVCEAEVAKLGAKVSKAKKREALIACIEPDR 219

Qy 327 RVEIEVKGYKEVVTQ 341
Db 220 RVDVKI---RSIVTR 231

RESULT 27
A81782
outer membrane class 4 protein precursor (rmpM) - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 09-Jul-2004
C;Accession: A37004
R;Klugman, K.P.; Gotschlich, E.C.; Blake, M.S.
Infect. Immun. 57, 2066-2071, 1989
A;Title: Sequence of the structural gene (rmpM) for the class 4 outer membrane protein o
trution of meningococcal strains that lack class 4 protein.
A;Reference number: A37004; MUID:89277523; PMID:2499543
A;Accession: A37004
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-240 <KLJ>
A;Cross-references: UNIPROT:P38367
C;Keywords: membrane protein

Query Match 13.8%; Score 251; DB 2; Length 240;
Best Local Similarity 36.3%; Pred. No. 1e-11;
Matches 62; Conservative 27; Mismatches 58; Indels 24; Gaps 4;

Qy 190 GQEDAAPVAPAPAPAEVATKH-----FTLKSDVLFNFNFKATLKPEGOQALDQLYT 241
Db 64 GDAVAAPEPEPEPAPVAVVEQAPQYVDETISLSAKTLFGFDKSLRAEAQNLKVLQ 123

Qy 242 QLSNMDPKDGSAAVLGYTDRIIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMES 301
Db 124 RLQGTNIQ--SVRVEGHTDFMGSDKYNQALSERRAYVAVVANNLVNGVPVSRISAVGLGES 181

Qy 302 NPVTGNTCD-----NVKARAALIDCLAPDRRVEIEVKGYKEVVTQ 341
Db 182 QAQMTQVCEAEVAKLGAKVSKAKKREALIACIEPDRRVDVKI---RSIVTR 229

RESULT 28
A81782
outer membrane protein class 4 NMA2105 [imported] - Neisseria meningitidis (strain Z2491
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: A81782
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81782
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-242 <PAR>
A;Cross-references: UNIPROT:P38367; GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB8533
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: rmpM; NMA2105

Query Match 13.7%; Score 250; DB 2; Length 242;
Best Local Similarity 32.8%; Pred. No. 1.3e-11;
Matches 64; Conservative 34; Mismatches 75; Indels 22; Gaps 5;

Qy 164 NNIGDA--GTGTRPDNGMLSLGVSYRFGQEDAAPVAPAP-----PAPEVATKHFTLS 217

Db 42 NNYGECWKYADKASQGVCEGDVAAPPEPEPEPAPVVVVEQAPYYVDETISLSA 101
Qy 218 DVLVFNFNKATLKEGQQALDQLYTLQSNMDDPGSGSAVVLGYTDRIGSEAYNQOLSEKRAQ 277
Db 102 KTLFGFDKSLRAEAQDNKLVLAQRIGQTNIQ--SVRVEGHTDFMGSKYNAQALSERRAY 159
Qy 278 SVVDYLVAKGIPAGKISARGMGESNPVTGNTCD-----NVKARAALIDCLAPDR 326
Db 160 VVANNLVSGVPVSRISAVGLGESQAQMTQVCEAEVAKLGAKVSKAKKREALIACIEPDR 219
Qy 327 RVEIEVKGKVEVVTQ 341
Db 220 RVDVKI---RSIVTR 231
RESULT 29
S20494
root adhesin - Pseudomonas fluorescens
C:Species: Pseudomonas fluorescens
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000
C:Accession: S20494
R.de Mot, R.; Proost, P.; van Damme, J.; Vanderleyden, J.
Mol. Gen. Genet. 231, 489-493, 1992
A:Title: Homology of the root adhesin of Pseudomonas fluorescens OE 28.3 with porin F of
A:Reference number: S20494; MUID:92167971; PMID:1538702
A:Accession: S20494
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-326 <MOT>
A:Cross-references: EMBL:X62168
C:Superfamily: outer membrane protein A
Query Match 13.3%; Score 243; DB 2; Length 326;
Best Local Similarity 27.7%; Pred. No. 6.2e-11;
Matches 86; Conservative 47; Mismatches 109; Indels 68; Gaps 13;
Qy 73 GRMAYKGSVDNGAFKAQ-GVQLTAKLGYPIITDLDI-----YTR-----LGGM 114
Db 32 GELFYKKQVNDVKHIEDGFGNPGARIGVFLTDDLNLNLSYKTNHTRNGDGTSGKIGGD 91
Qy 115 VVRADSKNGYASTGYSRSEHDTGVSPVAGG-----VEMAVTRDIAT-----RL 158
Db 92 TSSLTAQYHFGQAGVD-----SLRPYVEGGHQSGRGNVKGADGSHGSDQSTLAIGAGV 145
Qy 159 EYQWNNIT-GDAGTGTGTRP-DNG-----MLSLGYSYRFGQDDAAPVVAPAPAPAPE--- 207
Db 146 KYFTNNYVARAGVEADYALDNGKWDYSALVGLGVN--FGNAGGAAAPPTPAPAPETP 203
Qy 208 ----VATKHFTLKSDVLFNFKATLKPEGQQALDQLYTLQSNMDPKGSAAVVLGYTDRIG 263
Db 204 EPEAPVAQVVRVELDVKDFDKSVKPNISYGDVKNLADFMQAQYPAT--NVEVAGHTDSIG 261
Qy 264 SEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLA 323
Db 262 PDAYNQKLSQRADRVKQVLYKDGVPASRITAVGYGESRPVADNATEAGR-----A 312
Qy 324 PDRRVEIEVK 333
Db 313 VNRRVEASVE 322
RESULT 30
S39156
outer membrane protein F precursor - Pseudomonas aeruginosa
N:Alternate names: porin F
C:Species: Pseudomonas aeruginosa
C:Date: 18-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: S39156; S39159; G83423
R.Duchene, M.; Schweizer, A.; Lottspeich, F.; Krauss, G.; Marget, M.; Vogel, K.; von Spe
J. Bacteriol. 170, 155-162, 1988
A:Title: Sequence and transcriptional start site of the Pseudomonas aeruginosa outer mem
A:Reference number: S39156; MUID:88086862; PMID:2447060

A:Accession: S39156
A:Molecule type: DNA
A:Residues: 1-350 <DUC>
A:Cross-references: UNIPROT:P13794; EMBL:M18975; NID:g151507; PIDN:AAA25973.1; PID:g1515
A:Accession: S39159
A:Molecule type: protein
A:Residues: 25-37/39-53; 79-84; 189-202; 253-259; 261-267; 297-301/315-318; 325-334; 340-345 <Br
R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: G83423
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <STO>
A:Cross-references: GB:AE004603; GB:AE004091; NID:g9947751; PIDN:AAG05166.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: OprF; PA1777
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-350/Product: outer membrane protein F #status experimental <MAT>
Query Match 12.7%; Score 231.5; DB 2; Length 350;
Best Local Similarity 26.0%; Pred. No. 5.1e-10;
Matches 82; Conservative 43; Mismatches 87; Indels 103; Gaps 14;
Qy 97 LGYPITDLDIYTRLGGMVWRADSKGNYS-----HGVRTYETGNKKVHGNLTSLDAIYHFGTGVGLRPVVS 113
Db 57 IGYFLTDDVELALSYGEY---HDVVRTYETGNKKVHGNLTSLDAIYHFGTGVGLRPVVS 113
Qy 144 GGV-----EWAVTRDIATRLRYQWNNI-----GDAGTGTGTRDNG-- 179
Db 114 AGLAHQINITNNSQGRQQTMANIGAGLYFTENFFAKASLDQGYGL--EKRDNGHQ 171
Qy 180 ---MLSLGYSYRFGQDDAAPVVAPAPAPAPVAT-----SDSDNDGVDNVDKCPDTPANVTVDAN 210
Db 172 GEMWAGLGVGNFGGSKA---APAPEVADVSDSDNDGVDNVDKCPDTPANVTVDAN 227
Qy 211 -----KHFTLKSDFLNFNFKATLKPEGQQALDQLYTLQSLNM-----DPKDGSAVVLGYT 259
Db 228 GCPAAVEAVRVQLDVKDFDKSVK-----ENSADIKNLADFMKQYPTSTTVEGHT 280
Qy 260 DRIGSEAYNQOLSEKRAQSVVDYLVAK-GIPAGKISARGMGESNPVTGNTCDNVKARAAL 318
Db 281 DSVGTDAYNQKLSERRANAVRDVLNVEYGEGRVNAVGYGESRPV-----ADNATAEGRA 336
Qy 319 IDCLAPDRRVEIEVK 333
Db 337 I-----NRRVEAEVE 346
RESULT 31
H87341
OmpA family protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: H87341
R.Nierman, W.C.; DeBlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87341
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-407 <STO>
A:Cross-references: UNIPROT:Q9AA59; GB:AB005673; NID:g13421980; PIDN:AAK22732.1; GSPDB:G
C:Genetics:

as-Neto, E.; Docena, C.; El-Dorrry, H.; Pacincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kutamae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matakuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0343

Query Match 11.3%; Score 206; DB 2; Length 389;
Best Local Similarity 25.6%; Pred. No. 4.9e-08;
Matches 102; Conservative 46; Mismatches 142; Indels 108; Gaps 18;

Qy 4 IFVLNAAPKNTWYAGKLGWSQVHDTGYNGFNNGPTRND-----QLGAGAPGGYQV 59
Db 31 IQVASAQEFDRWYLAG-----STGF---NFQDKRRLT-NDAPFFTLGIGKF---I 74
Qy 60 NPYLGFENGYDWLGMWYKGVNDGAFKAQGVLTAKLGYPI-----TDDLDIYTR 110
Db 75 NPVMSID-----GTLNYQ-----NPQFSKNKDLNWSQYGFSDFRHFQIDNRGNPYLE 124
Qy 111 LCGMWMRADSKGNVASTGVSRSEHDTGVSPVFAG-GVEMAVTVRIATLREYQWNNIGDA 169
Db 125 LCAGYQSRSEEDFTNPANSGERKKGFAKVGAGLQTTFSRVATRAE---VAYRGDH 181
Qy 170 GTVQTR-PDNG-----MLSLGVSYRFGQEDAAFPVAPAP-----APAPEVATK 211
Db 182 DKDSVRQPVAGVAAAPSSKKWFGDTLASGVVIFPGPAAASPTPPAPAPTPPPPPAPS 241
Qy 212 HFTLKSD-----VLNFNKATLKPEGQOAL 236
Db 242 CAELDSBDGVDNCDCKPNSQPGQTIGDPCVPVSIIDLKGVNFDFDKSLRPDAVAVL 301
Qy 237 DOLYTLNSMPPDKGSVAVLVGTVDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGK-ISA 295
Db 302 KEA-TEILRRYP-DLHUEVAGHTOSTGPAATNKKLSERRAKVVDYLRNNGIDASRLIGP 359
Qy 296 RGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVK 333
Db 360 VGYGETHIDNTKTPAGRAK-----NRRTELNVQ 388

RESULT 35
A83516
probable outer membrane protein PA1041 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: A83516
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Latbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83516
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-210 <STO>
A;Cross-references: UNIPROT:Q914T3; GB:AE004536; GB:AE004091; NID:g9946945; PIDN:AAG0443
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA1041

Query Match 10.9%; Score 199; DB 2; Length 210;
Best Local Similarity 28.4%; Pred. No. 7.5e-08;
Matches 63; Conservative 29; Mismatches 64; Indels 66; Gaps 8;

Qy 125 ASTGVSRSEHDTGVSPVFAGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLG 184
Db 40 AGLGAIESSWAGNALIGGGVGAA-----YCWVHGAGEQ----- 74
Qy 185 VSYRFGQEDAAFPVAPAP-----APAPEVATKHFTLKSDVLNPNKATLKPEGQOALD 237
Db 75 -----VAPPPQPVVEVAPPPPVVKEETIVRDLHFAPFSSKVDAAADSEKLN 121
Qy 238 QLYTQLNSMPPDKGSV-----VLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGK 292
Db 122 GIAERLK-----GEASTRLSIITGHTDSVGSDAYNQKLSERRANAVANYLIDAGVPSSI 175
Qy 293 I-SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVK 333
Db 176 IVGVQGLGESQPVADN-----KTR-----EGRAENRRVEILIK 208

RESULT 36

D87682

OmpA family protein [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C;Accession: D87682

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: D87682

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-449 <STO>

A;Cross-references: UNIPROT:Q9A2R2; GB:AE005673; NID:gl3425220; PIDN:AAK25456.1; GSPDB:G

C;Genetics:

A;Gene: CC3494

Query Match 10.6%; Score 193.5; DB 2; Length 449;
Best Local Similarity 21.2%; Pred. No. 5.2e-07;
Matches 88; Conservative 55; Mismatches 133; Indels 139; Gaps 17;

Qy 1 MKALFVNAAPKONT-WYAGKLG-----WSQYHD-TGPGY 34
Db 59 LAAVFAASGVSAOETGWYGVADLQHWFPQSISTESNTLPDGBYAHWAWKTKDQWTFVR 118
Qy 35 NGFQNN-----GPTR---NDOLGA--GAFGG 56
Db 119 LGYQFNKNWRAEVEGGYRPGDLKAVRGNVRRQPVALCTPGVTRTSSQRCSPDGSDS 178
Qy 57 YQ-----VNPYLGFEMGYD-----WLGMAVYKGSVDNGAFKAQGVQLTAKL 97
Db 179 WSLMANVIYDFAPDSWLNPPFVAGVGNRLDVKTLGQFSGVAVTPGNVAQNLTV--- 234
Qy 98 GYPITDLDIYRLGGMWTRADSKGNVASTGVSRSEHDTGVSPVFAGVEWAVTRDIATR 157
Db 235 -----DDDDM-----AVAQAIAGASIKATKLKVD-----VTYRYLTG 268
Qy 158 LEYQWVNN---IGDAGTVGTRPDNGMLSLGVSYRFGQ-----EDAAAPV 198
Db 269 SDHSWSSGSLGLQPFAGSQYTDQSLTVGLRVSFASPPPPPPPPPPPPPPPPPPPP 328
Qy 199 APAPAPAPEVATKHFTLKSDVLNPNKATLKPEGQOALDQLYTQLNSMPPDKGSVAVLGY 258
Db 329 PPPPPPPPAFEAREFI---VYFPDQSVLTPEAQSVVTEA-AKYSN-DGKATKIIVVGH 382
Qy 259 TDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVK 313
Db 383 TDTSGSPKYNKLSERRARAVADALVSQVSNVLGVDWKGESAPAVA-TGDGVK 436

RESULT 37

S47773

hypothetical 22.2K lipoprotein (bisc-cspA intergenic region) - Escherichia coli (strain

N;Alternate names: hypothetical protein o219
C;Species: Escherichia coli
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S47773; B65154
R;Plunkett, G.
submitted to the EMBL Data Library, March 1994
A;Reference number: S47666
A;Accession: S47773
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <PLU>
A;Cross-references: UNIPROT:P37665; EMBL:U00039; NID:G466582; PIDN:AAB18529.1; PID:G4666
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B65154
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-219 <BLAT>
A;Cross-references: GB:A8000432; GB:U00096; NID:G2367241; PIDN:AAC76576.1; PID:G1789974;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: yiaD

Query Match 9.8%; Score 179; DB 2; Length 219;
Best Local Similarity 24.5%; Pred. No. 2.6e-06;
Matches 70; Conservative 36; Mismatches 90; Indels 90; Gaps 10;
Qy 50 GAGAFGGYQVNPYLGFEFGYDNLGRMAYKGSVDNGAFKAQGVLTAKLGYPIITDLDIYT 109
Db 14 GALAVSGCTTNPYTG-----EREAGKSAIGAG----- 40

Qy 110 RLGGMWRADSKGNVYASTG-VSRSEHDTGVPFAGGVEMAVTRDIATRLLEYQWV---N 165
Db 41 -LGLVSG-----AGIGALSSSKDKRGKCALICAAAGALGGGVYMDVQEANVRDK 91

Qy 166 IGDAGTGTGTRPDNGMLSLGVSYRFGQEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAP 225
Db 92 MRGTGVSVTRSGDNII-----LNMPNNVTFDSSS 120

Qy 226 ATLPEGOQALDQLYTQLSNMDPKDGSV-VLGYTDRIGSEAYNQOLSEKRAQSVVDVLY 284
Db 121 ATLPAAGANTLTGVAMVLKEY-PK--TAVNVVGYTDTSGHDLNRLSQQRADSVASALI 177

Qy 285 AKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEI 330
Db 178 TQGVDAISRITQGLGPANPIASNSTAEGKAQ-----NRRVEI 214

RESULT 38
E83185
Probable outer membrane protein PA3692 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: E83185
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bu
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83185
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-261 <STO>
A;Cross-references: UNIPROT:Q9HXU8; GB:AE004788; GB:AE004091; NID:G9949846; PIDN:AAG0708
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA3692

Query Match 9.7%; Score 176.5; DB 2; Length 261;
Best Local Similarity 24.5%; Pred. No. 2.6e-06;
Matches 70; Conservative 36; Mismatches 90; Indels 90; Gaps 10;

Best Local Similarity 36.5%; Pred. No. 5e-06;
Matches 42; Conservative 23; Mismatches 39; Indels 11; Gaps 3;
Qy 218 DVLFNFNKATLKPEGOQALDQLYTQLSNMDPKDGSVAVLGYTDRIGSEAYNQOLSEKRAQ 277
Db 143 DVLFDLKSDLKPGAMENIQQL-AEFLQONP-ERQVIVEGYTDTSGSYANTYQRLSERRAD 200

Qy 278 SVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 332
Db 201 SVRMALLSRGISPERVATRGYKGYPVASNGTSSGRAM-----NRRVEVTI 246

RESULT 39
AC0982
Probable outer membrane protein STY4157 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AC0982
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov.
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AC0982
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-220 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07983.1; PID:G16504969; GSPDB:GN00176
C;Genetics:
A;Gene: STY4157

Query Match 9.7%; Score 176; DB 2; Length 220;
Best Local Similarity 23.9%; Pred. No. 4.4e-06;
Matches 68; Conservative 34; Mismatches 95; Indels 88; Gaps 8;
Qy 50 GAGAFGGYQVNPYLGFEFGYDNLGRMAYKGSVDNGAFKAQGVLTAKLGYPIITDLDIYT 109
Db 14 GALAVSGCTTNPYTG-----EREAGKSGIGAGISLVGAGIGA----- 51

Qy 110 RLGGMWRADSKGNVYASTGVSRSSEHDTGVPFAGGVEMAVTRDIATRLLEYQWV---NNI 166
Db 52 -----LSSKKDRGKCALICAAAGALGGGVYMDVQEAKLKDKM 92

Qy 167 GDAGTGTGTRPDNGMLSLGVSYRFGQEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAP 226
Db 93 RGTGVSVTRSGDNII-----LNMPNNVTFDSSA 121

Qy 227 TLKPEGOQALDQLYTQLSNMDPKDGSV-VLGYTDRIGSEAYNQOLSEKRAQSVVDVLYA 285
Db 122 TLKPAGANTLTGVAMVLKEY-PK--TAVNVVGYTDTSGHDLNRLSQQRADSVASSLIT 178

Qy 286 KGIIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEI 330
Db 179 QGVDAISRITSGMGFANPIASNSTAEGKAQ-----NRRVEI 214

RESULT 40
E91183
Probable outer membrane protein ECG4437 [imported] - Escherichia coli (strain O157:H7, s
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: E91183
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E91183
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-219 <HAY>
A;Cross-references: UNIPROT:O8XDP2; UNIPROT:Q8CVK6; GB:BA000007; PIDN:BA037860.1; PID:gl
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs4437

Query Match 9.5%; Score 174; DB 2; Length 219;
Best Local Similarity 24.1%; Pred. No. 6.1e-06;
Matches 69; Conservative 37; Mismatches 90; Indels 90; Gaps 10;
QY 50 GAGAFGGYQVNPYLGFENGWLGWMAVKGSDNGAFKAAQGVQLTAKLGYPTDLDIYT 109
DB 14 GALAVSGCTTNPYTG-----EREAGKSAIGAG----- 40
QY 110 RLGGMWVRADSKGNVASTG-VSRSEHDTGVSVPFAGGVWAVTRDIATRLVEYQWV---NN 165
DB 41 -LGSLVG-----AGIGALSSSKKDRKGALIGAAAGALGGGVGYMDVQEAKLKRD 91
QY 166 LGDAGTGTGTRPDNGMLSLGVSYRFGQEDAAFPVAPAPAPAEVATKHTFLKSDVLFPNFK 225
DB 92 MRGTGVSVTRSGDNI-----LNMFPNVTFDSSS 120
QY 226 ATLKPEGQQAALDQLYTQLSNMDPKDGSV-VLGYTDRIGSEAYNQOLSEKRAQSVVDYLV 284
DB 121 ATLKPAGANTLTGVAMVLKEY-PK--TAVNIGYDSTGCHDLNRLSQRADSVASALI 177
QY 285 AKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEI 330
DB 178 TQGVDSASRTQGLGPANPIASNSTAEGKAQ-----NRRVEI 214

RESULT 41
A86030
probable outer membrane protein yiaD [imported] - Escherichia coli (strain O157:H7, sube
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: A86030
J;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamasis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A86030
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <STO>
A;Cross-references: UNIPROT:O8XDP2; UNIPROT:Q8CVK6; GB:AE005174; NID:g12518287; PIDN:AA
A;Experimental source: strain O157:H7, substrain EDU933
C;Genetics:
A;Gene: yiaD

Query Match 9.5%; Score 174; DB 2; Length 219;
Best Local Similarity 24.1%; Pred. No. 6.1e-06;
Matches 69; Conservative 37; Mismatches 90; Indels 90; Gaps 10;
QY 50 GAGAFGGYQVNPYLGFENGWLGWMAVKGSDNGAFKAAQGVQLTAKLGYPTDLDIYT 109
DB 14 GALAVSGCTTNPYTG-----EREAGKSAIGAG----- 40
QY 110 RLGGMWVRADSKGNVASTG-VSRSEHDTGVSVPFAGGVWAVTRDIATRLVEYQWV---NN 165
DB 41 -LGSLVG-----AGIGALSSSKKDRKGALIGAAAGALGGGVGYMDVQEAKLKRD 91
QY 166 LGDAGTGTGTRPDNGMLSLGVSYRFGQEDAAFPVAPAPAPAEVATKHTFLKSDVLFPNFK 225
DB 92 MRGTGVSVTRSGDNI-----LNMFPNVTFDSSS 120
QY 226 ATLKPEGQQAALDQLYTQLSNMDPKDGSV-VLGYTDRIGSEAYNQOLSEKRAQSVVDYLV 284
DB 121 ATLKPAGANTLTGVAMVLKEY-PK--TAVNIGYDSTGCHDLNRLSQRADSVASALI 177
QY 285 AKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEI 330

Db 178 TQGVDSASRTQGLGPANPIASNSTAEGKAQ-----NRRVEI 214
RESULT 42
A83541
hypothetical protein PA0833 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: A83541
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 953-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83541
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-237 <STO>
A;Cross-references: UNIPROT:Q915A7; GB:AE004518; GB:AE004091; NID:g9946725; PIDN:AAG042
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0833

Query Match 9.5%; Score 173.5; DB 2; Length 237;
Best Local Similarity 26.9%; Pred. No. 7.4e-06;
Matches 52; Conservative 29; Mismatches 81; Indels 31; Gaps 7;
QY 164 NNIGDAGTGTGTRPDNGMLSLGVSYRFGQEDAAFPVAPAPAPAEVATKHTLK----SDV 219
DB 62 NNRKGALIGAIV-AGAAAAGYGY-YADKQAEALRRQMEGTGVEVQRGGDDIKLIMPNI 119
QY 220 LFENFKATLKPEGQQAALDQLYTQLSNM-----DPKDGSAVVLYGTDRIGSEAYNQOLSEK 274
DB 120 TFAIDSANIAP-----SFVAPLNLANSPKQYNQNTIEIVGYTDSGSRQHNWDLQR 172
QY 275 RAQSVVDYLVAKGIPAKGISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVK- 333
DB 173 RAQSVAGYLTAAQGVDTGRLTSGMGDPQPIASN-----STADGQAQNRREVNLRP 223
QY 334 ---CYKEVVTQPP 343
DB 224 VPGAQGAQPAQTQPP 236

RESULT 43
H70782
probable ompA protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70782
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70782
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-326 <COL>
A;Cross-references: UNIPROT:Q10557; GB:Z73101; GB:AL123456; NID:g3261565; PIDN:CAA97374.
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: ompA

Query Match 9.5%; Score 173.5; DB 2; Length 326;
Best Local Similarity 28.6%; Pred. No. 1.1e-05;
Matches 62; Conservative 31; Mismatches 91; Indels 33; Gaps 8;
QY 129 VSRSEHDTGVSVPFAGGVWAVTRDIATRLVEYQWNVNIGDA-----GTVGTRPD 177

Db 129 VVRSIDPSSAEPVFTASVP---IPDFGLKVERDVTTLTGTA PPSSEHKDAVKRAATSTWPD 185

Qy 178 NGML-SLGVSYRFGQEDAAPVAPAPAPAPAPAVATK-HFTLKS DVLFPFNKATLKPEGQQA 235

Db 186 MKIVNNIEVT---GQ---APGPPASGCDLQSAINAVTGGPIAFGNDGASLIPADYEI 239

Qy 236 LDQLYTQLSNMDPKDGSAYVLGYDTRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISA 295

Db 240 LNRVADKLKAC--PDARVTINGYDNTGSEGINPLSAQRAKIVADYLVARGVAGDHIAT 297

Qy 296 RGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 332

Db 298 VGLGSVNPFIASNA TPESGRAK-----NRRVEIVV 325

RESULT 44

H95302

probable membrane protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid

C:Species: Sinorhizobium meliloti

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C:Accession: H95302

R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows

.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

C:Contents: annotation

C:Genetics:

A:Gene: Sma0626

A:Genome: plasmid

Query Match 9.4%; Score 171.5; DB 2; Length 420;

Best Local Similarity 30.2%; Pred. No. 2.2e-05;

Matches 51; Conservative 27; Mismatches 64; Indels 27; Gaps 4;

Qy 178 NGMLSLGVSYRFGQEDAAPVAPAPAPAPAPAVATK-HFTLKS-----DVLFP 221

Db 24 NASLCEGVARKLLMAGALVAATNVPWCWSQSVADPVKQYSKESMQOALQTRREQYDVHGLSF 83

Qy 222 NFNKATLKPEGQQAALDQLYTQLSNMDPKDGSAYVLGYDTRIGSEAYNQOLSEKRAQSVVD 281

Db 84 DTGQSTLQPGAKPLDLDIATALKNF--PDWSLRIVGHTDASGSAESNERLSLERANTIKA 141

Qy 282 YLVAKGIPAGKISARGMESNPVTGNTCDNVKARAALIDCLAPDRRVEI 330

Db 142 ALVERGIDAGKLLAAGAGQSRPIASNETDEGKAL-----NRRVEL 181

RESULT 45

C82230

probable lipoprotein VCI195 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: C82230

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: C82230

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-223 <HEI>

A:Cross-references: UNIPROT:Q9KSR1; GB:AE004199; GB:AE003852; NID:g9655666; PIDN:AAF9435

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VCI195

A:Map position: 1

Query Match 9.3%; Score 170; DB 2; Length 223;

Best Local Similarity 28.8%; Pred. No. 1.3e-05;

Matches 62; Conservative 35; Mismatches 90; Indels 28; Gaps 8;

Qy 125 ASTGVSRSSEHDT--GVSPVPAGGVEWAVTRDIA--TRLEYQWVNNIGDAGTVGTRPDNGML 181

Db 26 ATTGETETNATTKGALLGVLAGAAGLGTGDGAKERRKHALIGAAGGA VGG----- 77

Qy 182 SLGVSYRFGQEDA--APVAPAPAPAPAVATKHTFLKSD--VLFNFKATLKPEGQQA LD 237

Db 78 --GGIYFDQQAELRKALDSDGVVVVRVGENQMLNRNENGIGFTS YQLDSDVIHKTLR 135

Qy 238 QLYTQLSNMDPKDGSAYVLGYDTRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARG 297

Db 136 GVARIL--VEYPTDSLVIEGHTDSTGSDTTNQVLSKRAESVRSFLLSQGVAAGRAIARG 193

Qy 298 MGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 332

Db 194 NGERFPLCSN--NTAEGRAC-----NRRVEIQI 219

RESULT 46

B82815

conserved hypothetical protein XF0363 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: B82815

R:anonymou, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: B82815

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-242 <SIM>

A:Cross-references: UNIPROT:Q9PGD9; GB:AE003888; GB:AE003849; NID:g9105187; PIDN:AAF8317

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camaro, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshakho, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF0363

Query Match 9.3%; Score 169.5; DB 2; Length 242;

Best Local Similarity 24.5%; Pred. No. 1.5e-05;

Matches 59; Conservative 38; Mismatches 85; Indels 59; Gaps 8;

Qy 112 GGMVWRADSKGNVASTGVSRSEHDTGVSPFAGGVEWAVTRDIATRLLEYQWVNNIGDAGT 171

Db 27 GGSVQRDQSGN--STEQNRNTRGRDAICAAI--GAAAGLLTGKNTAK----- 70

[illegible]

C;Genetics:
A;Gene: VCA0659
A;Map position: 2

```
Q7      ||| : | - : | - : |  
255 GGGG T VGN CGN KKKKHHHHDLCDFRRVEI   350  
  
Db     178 GENVPACTNSTYKNGRA-----C---NRVET 200
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Query Match	7.0%	Score 127.5;	DB 2;	Length 167;
Best Local Similarity	33.6%;	Pred. No. 0.014;		
Matches 38;	Conservative	20;	Mismatches 38;	Indels 17;
				Gaps 5;

R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, T.; Connerton, P.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, T.

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40346
R;Tibor, A.; Weynants, V.; Denoel, P.; Lichtfouse, B.; De Bolle, X.; Saman, E.; Limet, J.
Infect. Immun. 62, 3633-3639, 1994
A;Title: Molecular cloning, nucleotide sequence, and occurrence of a 16.5-kilodalton out
A;Reference number: I40346; MUID:94341863; PMID:8063379
A;Accession: I40346
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-168 <RES>
A;Cross-references: UNIPROT:Q44662; GB:L27996; NID:g619644; PIDN:AAA59360.1; PID:g538293
C;Genetics:
A;Gene: pal
C;Superfamily: outer membrane protein A

Query Match 6.7%; Score 122; DB 2; Length 168;
Best Local Similarity 23.4%; Pred. No. 0.037;
Matches 39; Conservative 26; Mismatches 54; Indels 48; Gaps 7;

Qy 164 NNIGDAGTVGTRPDNGMLSLGVSRFGQEDAAPVAPAPAPAPAEVATKGFHLK--SDVLF 221
Db 33 NNAGDLG-----LG-----AGATPG-----SSQDFTVNVGDRIF 63

Qy 222 NFNKATLKPEQQQALD-----QLYTQLSNMDPKDGSAAVLGYTDRIKSEAYNQQLSEKR 275
Db 64 DLDSLLIRADAQTLKQAQWLQRYQY-----SITISGHADRGTRREYNLALGQRR 115

Qy 276 AQSVDVYLVAKGIKAGKISARGMESNPVT---GNTCDNVKARAALI 319
Db 116 AAATRDFLASRGVPTNRMTISYGNERVAVCDADTCWQSNRRVAV 162

RESULT 81
I39802
motB protein homolog - Bacillus megaterium
C;Species: Bacillus megaterium
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: I39802
R;Hueck, C.; Kraus, A.; Hillen, W.D.R.
Gene 143, 147-148, 1994
A;Title: Sequences of ccpA and two downstream Bacillus megaterium genes with homology to
A;Reference number: I39800; MUID:94259294; PMID:8200532
A;Accession: I39802
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-218 <RES>
A;Cross-references: UNIPROT:P46827; GB:L26052; NID:g415663; PIDN:AAA22297.1; PID:g415666
C;Genetics:
A;Start codon: GTG
C;Superfamily: probably motility protein ytxE

Query Match 6.6%; Score 121; DB 2; Length 218;
Best Local Similarity 31.9%; Pred. No. 0.062;
Matches 43; Conservative 21; Mismatches 47; Indels 24; Gaps 7;

Qy 215 LKSDVLFNFKATLKPEQQQALDQLYTQLSNMDPKDGSAAVLGYTDR--IGSEAY--NQQ 270
Db 102 LQEQVLFETGQADILKGTTPDELGRFLFTI--PND--IKVEGHTDNRPIHTYAPSNWE 158

Qy 271 LSEKRAQSVVDYLVAK-GIPAGKISARGMESNPVTGNTCDNVKARAALIDCLAPDRRVE 329
Db 159 LSAARASGVIRYLTNHFSLSANRFEALGYGDTKPLVPNTSN-----DNLQKNRVE 209

Qy 330 IEVKGYKEVVTQQA 344
Db 210 I-----IISDPEA 217

RESULT 82
G71344
probable outer membrane protein tpm50 - syphilis spirochete
N;Alternate names: antigen tpp57
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: G71344; S61867
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khaliq, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: G71344
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-417 <COL>
A;Cross-references: UNIPROT:P38369; GB:AE001209; GB:AE000520; NID:g3322547; PIDN:AAAC6527
A;Experimental source: strain Nichols
R;Cox, D.L.; Akins, D.R.; Porcella, S.F.; Norgard, M.V.; Radolf, J.D.
Mol. Microbiol. 15, 1151-1164, 1995
A;Title: Treponema pallidum in gel microdroplets: a novel strategy for investigation of
A;Reference number: S61867; MUID:95349399; PMID:7623668
A;Accession: S61867
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-126,128-349, 'E', 351-417 <COX>
A;Cross-references: EMBL:L28427; NID:g532657; PIDN:AAA99311.1; PID:g532658
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C;Genetics:
A;Gene: tpp57; TP0292
A;Start codon: GTG

Query Match 6.6%; Score 121; DB 2; Length 417;
Best Local Similarity 19.4%; Pred. No. 0.14;
Matches 76; Conservative 52; Mismatches 132; Indels 132; Gaps 15;

Qy 5 FVLNAPKDNWTYAGGKLGWSQVHDTGFGYGNFGQNNNGPTRNDQLGAGAGGYGVN--- 60
Db 91 FMTSEKSPNNTF-----RMRHYESIFWRD-----AFGVYDIDRSFF 127

Qy 61 -----PYLGFEMGYDM-----LGRMAYKGSVDNGAF 86
Db 128 MPVVRNVVPFDYDIEVGDTEHEAEAEHDLRDGFIQTFFIVFTVYTYRGEVQGSR 187

Qy 87 KAQGVQITAKGYPIITDDLIYTRLGWVRADSKGNVASTGVSRSRSHDTGVSVPFAGGV 146
Db 188 RYHHTTAAYSMYS-----ESPKRTHGVQRNAKE-GMPYVRTTGV 225

Qy 147 EWAVTRDIATRLVYQVWNNIGDAGTVGTRPDNG---MLSLGVSYRFGQEDAAPVAPAP 202
Db 226 -----SKQNDYWDNELGN---IAEYDDEFRLLYLSGGTVLRYQGTATAKNFAPER 273

Qy 203 -APAPEVATKHFHTLK-----SDVLFNFKATLKPEQQQALDQLYT 241
Db 274 FDPARTVVEQLQETLKLHMPDAKYRETEEGVTISIENVQPDADGASLAPSEYKLRKI-A 332

Qy 242 QLSNMDPKDGSAAVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKG-IPAGKISARGMGE 300
Db 333 ELLRAFP-DRELLVSGHAARRGSVQDQRISEERADVARYLOELGVVDDAAHVYTRGCGA 391

Qy 301 SNPTVGTCDNVKARAALIDCLAPDRVEIEV 332
Db 392 QQSIAPNDSDEGRKK-----NRRVEITI 414

RESULT 83
AE3013
cmplp protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AE3013
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, E.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.

A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AE3013
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-177 <KUR>
A:Cross-references: UNIPROT:Q8U9L5; GB:AE008689; PIDN:AAL44523.1; PID:gi7742135; GSPDB:C58
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: palA
A:Map position: linear chromosome
C:Superfamily: outer membrane protein A

Query Match 6.6%; Score 120.5; DB 2; Length 177;
Best Local Similarity 26.6%; Pred. No. 0.051;
Matches 29; Conservative 24; Mismatches 45; Indels 11; Gaps 3;

Qy 219 VLFNFNFKATLKPEGOQALDQLYTQLSNMDPKDGSAAVLGYTDRIQSEAYNQOLSEKRAQS 278
Db 70 IFPDDTSTIRADAQQTQROQWLSRY--PNYAITVEGHADERTREYNALGARRAAA 127

Qy 279 VVDYLVKAGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRR 327
Db 128 TRDFLASQGVPSARMKTTISYGKEKPA--VCDD-----ISCWSQNR 167

RESULT 84
B98271
omp16 protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: B98271
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B98271
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-177 <KUR>
A:Cross-references: UNIPROT:Q8U9L5; GB:AE007870; PIDN:AAK89692.1; PID:gi15159600; GSPDB:C58
C:Genetics:
A:Gene: AGR_L_2246
A:Map position: linear chromosome
C:Superfamily: outer membrane protein A

Query Match 6.6%; Score 120.5; DB 2; Length 177;
Best Local Similarity 26.6%; Pred. No. 0.051;
Matches 29; Conservative 24; Mismatches 45; Indels 11; Gaps 3;

Qy 219 VLFNFNFKATLKPEGOQALDQLYTQLSNMDPKDGSAAVLGYTDRIQSEAYNQOLSEKRAQS 278
Db 70 IFPDDTSTIRADAQQTQROQWLSRY--PNYAITVEGHADERTREYNALGARRAAA 127

Qy 279 VVDYLVKAGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRR 327
Db 128 TRDFLASQGVPSARMKTTISYGKEKPA--VCDD-----ISCWSQNR 167

RESULT 85
A28543
peptidoglycan-associated lipoprotein precursor - Haemophilus influenzae
N:Alternate names: outer membrane protein P6 precursor; protein OMPg
C:Species: Haemophilus influenzae
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004
C:Accession: A28543; A27558; E64064
R:Deich, R.A.; Metcalf, B.J.; Finn, C.W.; Farley, J.E.; Green, B.A. J. Bacteriol. 170, 489-498, 1988
A>Title: Cloning of genes encoding a 15,000-dalton peptidoglycan-associated outer membrane protein
A:Reference number: A28543; MUID:88115138; PMID:2828309
A:Accession: A28543
A:Molecule type: DNA

A:Residues: 1-153 <DEI>
A:Cross-references: UNIPROT:P10324; GB:IM18878; NID:gi148859; PIDN:AAA24940.1; PID:gi148860
A:Experimental source: Rd strain KW20
R:Nelson, M.B.; Apicella, M.A.; Murphy, T.F.; Vankeulen, H.; Spotila, L.D.; Rekosh, D. Infect. Immun. 56, 128-134, 1988
A>Title: Cloning and sequencing of Haemophilus influenzae outer membrane protein P6.
A:Reference number: A27558; MUID:88085463; PMID:3257200
A:Accession: A27558
A:Molecule type: DNA
A:Residues: 1-153 <NEL>
A:Cross-references: GB:M19391; NID:gi148960; PIDN:AAA24994.1; PID:gi148961
A:Experimental source: strain NTHI 1479 (non-typeable)
R:Flaischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Gubermann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A. Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: E64064
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-153 <TIGR>
A:Cross-references: GB:U32722; GB:L42023; NID:gi1573348; PIDN:AAC22039.1; PID:gi1573351; TIGR
A:Experimental source: Rd strain KW20
C:Superfamily: outer membrane protein A
C:Keywords: lipid binding; lipoprotein; membrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-153/Product: peptidoglycan-associated lipoprotein #status predicted <MAT>

Query Match 6.6%; Score 120; DB 2; Length 153;
Best Local Similarity 27.7%; Pred. No. 0.046;
Matches 41; Conservative 22; Mismatches 63; Indels 22; Gaps 5;

Qy 161 QWVNICDAGTVG-----TRPDNGMLSLGVSRYFGQEDAAPVAPAPAPAEVATKHFTL 215
Db 3 KPVLSLLVAGSVAALAACSSNNDAAGAAQTGGYSVA-----DLQORYNT- 50

Qy 216 KSDVLFNFNFKATLKPEGOQALDQLYTQLSNMDPKDGSAAVLGYTDRIQSEAYNQOLSEKR 275
Db 51 ---VYFGPKDYDTGEEVQILD-AHAAYLNATPA-AKVLVEGNTDERTGTPENIALGQRR 105

Qy 276 AQSVDYLVKAGIPAGKISARGMGESNP 303
Db 106 ADAVKYGLAGKGVDAKGLGTVSYGEEK 133

RESULT 86
AH2184
hypothetical protein all3031 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AH2184
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH2184
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-599 <KUR>
A:Cross-references: UNIPROT:Q8YSQ3; GB:BA000019; PIDN:BAW74730.1; PID:gi7132125; GSPDB:G58
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all3031

Query Match 6.6%; Score 119.5; DB 2; Length 599;
Best Local Similarity 23.0%; Pred. No. 0.3;
Matches 44; Conservative 35; Mismatches 69; Indels 43; Gaps 6;

Qy 163 VNNIGDAGTVGTRPDNGMLSLGVSRY-----RFGQEDAAPVAPAPAPAEVATKHFTL 215

Db 422 IDHNGVLVAVGSAFQWILATKSWVIPGLTQFQDQL-----VSESLNELAIYQSOI 475
Qy 216 KSDVLVFNFNKATLXPEGQO-----ALDOLYTQLSNMNP-----KDGSAVVLGYTDR 261
Db 476 BREIIF-----FPEGSQEIIPSELSKLNLLVLAIKKLLPTIAKYLEKDVHIQIIGHTNT 528
Qy 262 IGSEAYNOLSEKRAQSVVDVLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDC 321
Db 529 TGTESRNQLSAGRSQRLVLSLSSQISTSQLVLGVSSSQFLOPELTDEGKXF----- 582
Qy 322 LAPDRRVEIEV 332
Db 583 ---NRRVSFKV 590
RESULT 87
AB0870
outer membrane protein (associated with virulence) STY3179 [imported] - Salmonella enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AB0870
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-178 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD02858.1; PID:g16504111; GSPDB:GN00176
C:Genetics:
A:Gene: STY3179
C:Superfamily: phage lambda membrane protein lom
Query Match 6.5%; Score 118.5; DB 2; Length 178;
Best Local Similarity 24.5%; Pred. No. 0.073;
Matches 47; Conservative 31; Mismatches 83; Indels 31; Gaps 8;
Qy 4 IFVLNAAPK-----DNTWYAGGKLGWSQYHDTGFGYNGFQNNNGPTRNDQLGAGAFGYQ 58
Db 12 IVLSAAASPWNADNA--STFSLGYAQSH-----TNHAGTLRGVRLA-----NNYE 56
Qy 59 VNPYLGFEMGYDWL-GRMAYKGSVDNGAFKAQGVOLTAKLGYPTITDLDIYTRLGGMVWR 117
Db 57 MSPDWGLTTSFAWLNGSQRYSDSSNGRVTTRYISLLAGPSWKINNQLSLYSQVGPVLH 116
Qy 118 ADSKGNAYSTGVSSEHTDGVSPFAGGVEMAVTRDIATRLLEYQWNNIGDAGTVGTRPD 177
Db 117 ORDHG-----INESDSKVGYSAGVAYTPVSNVAITLGYEGA-DFDATHNSGSLNS 167
Qy 178 NGMLSLGVSYRF 189
Db 168 NG-FNLGVGYRF 178
RESULT 88
AG2841
outer membrane protein omp [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AG2841
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Katp, P.; Romero, P.; Zhang, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, G.; Gillet, W.; Grant, C.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AG2841
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-209 <KUR>
A:Cross-references: UNIPROT:Q8UDG6; GB:AB008688; PIDN:AAL43149.1; PID:g17740625; GSPDB:G17740625; strain C58 (Dupont)
C:Genetics:
A:Gene: omp
A:Map position: circular chromosome
Query Match 6.4%; Score 117.5; DB 2; Length 209;
Best Local Similarity 25.4%; Pred. No. 0.11;
Matches 52; Conservative 23; Mismatches 65; Indels 65; Gaps 13;
Qy 15 TW----YAG--GKLQWSQYHDTGFGYNGFQNNNGPTRNDQLG---GAFGGYQV----- 59
Db 40 TWSGPLYGIQGGAGWA-----NGDFSAGGPPVSDDFNNGGILGAFAGYNYOFDNNMV 90
Qy 60 -----NPLYGFEMGYDWLGRMAYKGSVDNGAFKAQGVOLTAKLGYPTITDLD 106
Db 91 LGIEGDVDYNNWNDYSGIKVGTDWQ-----SVRGRVGYAF-DHAL 131
Qy 107 IYTRLGGMVWRADSKGNAYSTGVSSEHTDGVSPFAGGVEMAVTRDIATRLLEYQWNNI 166
Db 132 IYATAG---WTA-TRG-FIETPVG-DDKATFNGYTVGAGVDYAFDTNVFGRLETRY-NDY 184
Qy 167 GDAGTVG--TRPDNGMLSLGVSYRF 189
Db 185 GDKDIFGINTDFDQHTVKVGLGVKVF 209
RESULT 89
H97618
25K outer-membrane immunogenic protein precursor AGR_C_3918 [imported] - Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: H97618
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-219 <KUR>
A:Cross-references: UNIPROT:Q8UDG6; GB:AB007869; PIDN:AAK87905.1; PID:g15157301; GSPDB:G15157301; strain C 3918
C:Genetics:
A:Gene: AGR_C_3918
A:Map position: circular chromosome
Query Match 6.4%; Score 117.5; DB 2; Length 219;
Best Local Similarity 25.4%; Pred. No. 0.11;
Matches 52; Conservative 23; Mismatches 65; Indels 65; Gaps 13;
Qy 15 TW----YAG--GKLQWSQYHDTGFGYNGFQNNNGPTRNDQLG---GAFGGYQV----- 59
Db 50 TWSGPLYGIQGGAGWA-----NGDFSAGGPPVSDDFNNGGILGAFAGYNYOFDNNMV 100
Qy 60 -----NPLYGFEMGYDWLGRMAYKGSVDNGAFKAQGVOLTAKLGYPTITDLD 106
Db 101 LGIEGDVDYNNWNDYSGIKVGTDWQ-----SVRGRVGYAF-DHAL 141
Qy 107 IYTRLGGMVWRADSKGNAYSTGVSSEHTDGVSPFAGGVEMAVTRDIATRLLEYQWNNI 166
Db 142 IYATAG---WTA-TRG-FIETPVG-DDKATFNGYTVGAGVDYAFDTNVFGRLETRY-NDY 194
Qy 167 GDAGTVG--TRPDNGMLSLGVSYRF 189
Db 195 GDKDIFGINTDFDQHTVKVGLGVKVF 219

RESULT 90
AC3615
31K outer-membrane immunogenic protein precursor BMEII0844 [imported] - Brucella melitensis
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AC3615
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, E.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AC3615
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-219 <KUR>
A:Cross-references: GB:AB008918; PIDN:AAL54086.1; PID:gi7985044; GSPDB:GN00191
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEII0844
A:Map position: 11

Query Match 6.4%; Score 116; DB 2; Length 219;
Best Local Similarity 25.0%; Pred. No. 0.15;
Matches 55; Conservative 34; Mismatches 81; Indels 50; Gaps 10;

Qy 9 AAPKNTWYAGKLGWSQYHDTGFGNGF-----QNNNGPTRNDQLGAGAFGGYQVNPYL 63
Db 11 AAPVDTFSGYIGINAGYAGGPKHPFSSFDKEDNEQVSGSLDVTAGGFVG-----63

Qy 64 GFENGWD-----LGR-----MAYKGSVDNGAFKAGQVLT-----AKLGYPI 101
Db 64 GVQAGYNQDLONGVVLGAETDFQGSSTVTSISAGASGLEGAETKVEWFGFTRARLGYTA 123

Qy 102 TDDDIYTRLG---GMVWRADSKGYASTGVSRSSEHDTGSPVFAGGVEWAVTRDIATRL 158
Db 124 TERLMVYGTGLAYGVKVSANFLGDDASALHTWSD-KTKACWTLCAGAEYAINNNWLKS 182

Qy 159 EYQWNNIGDAGTVGTRPDNGMLS-----LGVSYRF 189
Db 183 EYLV-TDLGKRLNDV--DNSFLESKVNFTVRVGLNYKF 219

RESULT 91
AG3480
25K outer-membrane immunogenic protein precursor [imported] - Brucella melitensis (strain
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AG3480
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, E.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AG3480
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-228 <KUR>
A:Cross-references: UNIPROT:Q8YBP9; UNIPROT:Q8G333; GB:AE008917; PIDN:AAL53010.1; PID:gi7985044
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEII829
A:Map position: 11

Query Match 6.3%; Score 114.5; DB 2; Length 228;
Best Local Similarity 22.0%; Pred. No. 0.2;
Matches 47; Conservative 33; Mismatches 69; Indels 65; Gaps 11;

Qy 15 TW---YAGCKLGWS-----QYHDTGFGNGFQNNNGPTRNDQLGAGAFGGYQVN-----60
Db 41 TWNGAYLGGQIGYANGKSHFSYDSTGL-----GDIKPDGFLGGLYAGYNFDLGNV 91

Qy 61 -----PYLGFENGVDWL-----GRMAYKGSVDNGAFKAGQVLTAKLGYPI 102

Db 92 VLGIDGVTYNDVSKNIDFLDENNAATFNRLWSGAV-----RARGVAVD 139

Qy 103 DDLIYTRLGGWVRA-DSKNYASTGVSRSSEHDTGSPVFAGGVEWAVTRDIATRL 161
Db 140 RFLPYIA--GGVAFGSLNRGEPGSGTQSKTLTGMT--IGAGWDYAATDNVILRL 195

Qy 162 WVN-----NIGDAGTVGTRPDNGMLSGLGSYRF 189
Db 196 YTDYGNKDYGFDDAAVTNNFKTND-IRFGVAYKF 228

RESULT 92
S21596
extracellular protein precursor, 57K - Renibacterium salmoninarum
C:Species: Renibacterium salmoninarum
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S21596
R:Chien, M.S.; O'Hara, P.J.; Landolt, M.L.; Winton, J.R.
submitted to the EMBL Data Library, June 1992
A:Description: Sequence analysis of the 57-kilodalton soluble antigen of Renibacterium
A:Reference number: S21596
A:Accession: S21596
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-557 <CHI>
A:Cross-references: UNIPROT:Q00876; EMBL:Z12174; NID:g46408; PIDN:CAA78165.1; PID:g46409

Query Match 6.3%; Score 114; DB 2; Length 557;
Best Local Similarity 25.1%; Pred. No. 0.71;
Matches 57; Conservative 19; Mismatches 63; Indels 88; Gaps 15;

Qy 9 AAPKNTWYAGKLGWSQYHDTGFGNGFQ-----NNG--PTRNDQ 48
Db 334 ATPVTGKWSG-----DNNYTGKFWKDGQVWLQKPNAGSVSVAFGNPGDPTVTGDW 384

Qy 49 LGAGAFGGYQVNPYLGFEMGYDNLGRMAYKGSVDNGAFKAGQVLTAKLG-YPITDLDLI 107
Db 385 DGKGRFG-----IGVERGGW-----YLSNAGTSIGKVTAIVAFGNPGDPTVTGD---429

Qy 108 YTRLGGWVRADSKGYASTGVSRSSEHDTGSPVFAGGVEWAVTRDIATR---LEYQWV- 163
Db 430 -----W-DGKKG-TSIGVTRST-----ANGLEWYITSLTANPPVSYHFIF 469

Qy 164 -----NNIGDAGT-VGTRPDNGMLSGLGSYRFQEDAAPVVA 199
Db 470 GNSTDAPITGNWIGTAKTQVGLHRENSIL---ISV-----DAQTVAS 508

RESULT 93
AD0359
probable membrane protein YPO2953 [imported] - Versinia pestis (strain CO92)
C:Species: Versinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AD0359
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tatrag, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, Nature 413, 523-527, 2001
A:Title: Genome sequence of Versinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AD0359
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-560 <KUR>
A:Cross-references: UNIPROT:Q8ZCM8; GB:AL590842; PIDN:CAC92199.1; PID:gl5980911; GSPDB:G
C:Genetics:
A:Gene: YPO2953

Query Match 6.2%; Score 113; DB 2; Length 560;
Best Local Similarity 28.1%; Pred. No. 0.85;
Matches 32; Conservative 26; Mismatches 42; Indels 14; Gaps 4;

Qy 220 LFNFNKATLPEGQQALDQLYQLSNM--DPKQGSVVLGYTDRIGSEAYNQQLSEKRAQ 277

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Db 441 LFDNSTKTLKNSQ--TNEMMWELLILVERNKEKKILLIVGHSNDTGTSSNMWMLSEQAL 498
Qy 278 SVVDYLVAKG-IPAGKISARGMGSNPVGTGTCNDVVARAALIDCLAPDRRVEI 330
Db 499 ALRDWLKRSITVDNFTITKMGASEPVATNHTAGREQ-----NRRVEV 543

RESULT 94
AE0138
peptidoglycan-associated lipoprotein Pal [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE0138
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Fitball, R.W.; Holden, M.T.G.; Prentice, M.B.
Geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AE0138
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-168 <KUR>
A:Cross-references: UNIPROT:Q8ZGZ0; GB:AL590842; PIDN:CAC89968.1; PID:gl5979192; GSPDB:C
C:Genetics:
A:Gene: pal
C:Superfamily: outer membrane protein A

Query Match 6.1%; Score 112; DB 2; Length 168;
Best Local Similarity 35.3%; Pred. No. 0.21;
Matches 30; Conservative 12; Mismatches 41; Indels 2; Gaps 2;
Qy 219 VLFNFKATLKEGQALDQLYTQLSNMDPKDGSVVLGYTDRTGSEAYNQQLSEKRAQS 278
Db 66 VYFGFDKYDIGSDFAQMLD-AHAAFLRSNPSD-KVVVEGHADRTGTPYNIALGERRASA 123
Qy 279 VVDYLVAKGIIPAGKISARGMESNP 303
Db 124 VKMYLQKGVSADQISIVSYGKEP 148

RESULT 95
AD3302
3ik outer-membrane immunogenic protein precursor [imported] - Brucella melitensis (strain
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AD3302
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A:Reference number: AD3252; PMID:11756688
A:Accession: AD3302
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-201 <KUR>
A:Cross-references: UNIPROT:Q8YIPI; GB:AE008917; PIDN:AAL51583.1; PID:gl7982306; GSPDB:C
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0402
A:Map position: I

Query Match 6.1%; Score 111; DB 2; Length 201;
Best Local Similarity 23.5%; Pred. No. 0.32;
Matches 52; Conservative 23; Mismatches 64; Indels 82; Gaps 10;
Qy 24 WSOYHDTGFGNGFQNNNGPTRNDOLGAGAGGGYGVNPLYLGFEMGYDWL-----GRM 75
Db 8 WSPYWAQDFSGS-----LDVTASGFGVGVA-----GYNWQLANGLVLGGEA 49
Qy 76 AYKGS-----VDNGAFKAQGV-----QLTAKLGYPIITDLDIYT 109
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Db 50 DFOGSTVKSLVDNGDLSDIGVAGNLGDSFGLTKTQWQFQVGTVRARLGTPTLRLMVY- 108
Qy 110 RLGGWVRADSKNYASTGVSRSEHDTGVS-----PVPAGGVEWAVTRDIATRL 158
Db 109 GTGGLA-----YGKVKTSLSDYDDGESFSAGNSKTKAGWTLGAGVEAVTNNWTLKS 160
Qy 159 EYQWVN-----NIGDAGTVGTRPDNGM----LSLGVSYRFF 189
Db 161 EYLYTDLGKRKSFNVIDEENVNINWKNVPHTVRLGLNYKF 201

RESULT 96
C83054
hypothetical protein PA4735 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: C83054
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: C83054
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1088 <STO>
A:Cross-references: UNIPROT:Q9HV64; GB:AE004887; GB:AB004091; NID:9950991; PIDN:AAG0812
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4735

Query Match 6.1%; Score 110.5; DB 2; Length 1088;
Best Local Similarity 20.6%; Pred. No. 3.1;
Matches 64; Conservative 47; Mismatches 101; Indels 99; Gaps 17;
Qy 51 AGAFGGYQVNP-VLGFEMGYDWLGRMAYKGSVDNGAFKA-----QGVQLTAKLGYPIITD 103
Db 784 SGKPGYIRKGRNLNLDHY-----QIERSQLKAENKVLLEGLQGEKVDSP--D 831
Qy 104 LDIIYTRLGGWVRADSKGN---YASTGVSRSSEHDTGVSVPFAGGVEWAVTRDI---ATR 157
Db 832 AVDLPEVKLAVALLK-DTKGNIDIQLPVAGDLNNPEFSVMPIV-----WQTLRLNLVLRVQ 885
Qy 158 LEQWVNNIGDGT-VGTRPDNGMLSLGVSYRFGQDAAPV----- 197
Db 886 APFKFIAGLAAGGNEDIGTVP-----FAAGSDELTPEAQANLDKLADALKERPAL 935
Qy 198 -----VAPAPAPAPEVATKHFTL-----KSDVLFNFNKATLKPEGOQA--LD 237
Db 936 RLEVEGVASAAADGPSIGAKRLELEYQNTYRMLOQRGDKVPSPDAKOLEVPENWQAPLLE 995
Qy 238 QLY-TQLSNMNP-----KDGSAVVLGYTDRTIGSEAYNQQLSEKRAQSVVDYL 283
Db 996 GIYRTRLKQPPAPBWKELSDSERTAKMREAVIASWAK---SÖVLLRQIGQARATRIKDYL 1052
Qy 284 VAKG-IPAGKI 293
Db 1053 VEKQLPDDRI 1063

RESULT 97
G82151
peptidoglycan-associated lipoprotein VC1835 [imported] - Vibrio cholerae (strain N16961)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: G82151
R:Heidelberg, J.F.; Eissen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833; PMID:10952301
```

[illegible]

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Qy      91 VQLFAKLGYPITDLDIIVTRLGGM-----VWRADSKG-----NYASTGVSV--RSE   133
Db      60 -----GYDSYDCDIINPDYNMADFREFMKAADARGIKVIIDLVLNHSSTHEAFPKES    112
Qy     134 HDTGVSP-----VFAGGVSWAVTR-----DIATRL    158
Db     113 RSSKTNPGRDYIIWREKPNNWSFFGGSAWEIDKLGTGEYYHVSFKAQEADLNWANPAVR    172
Qy     159 EYQ-----WVNIGDAGTVGTR-----PDNGMLSLSGYSYRF----GQEDAA    195
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Db 173 EIEQVLAFWLNE---GVAGFRLDVINNLTVLLEFPDPNPVVDNEMEHVYDRNQGLEQAL 228
Qy 196 PVVAP-----APAPAEVATKHFTLKSDVLFNFNFKATLKPEGQQALD--QL 239
Db 229 EQIAAFCKREREVLVGEISSDKLPETAKYSSKTMLDVTFNFGSV-----ELDDAQSV 283
Qy 240 YTQLSNMDP--KDGSAVVLGY---TDRIGSEAYNQQLSEKRAOSVVDYLVAKGIP 289
Db 284 FTTLNEMETALQEGQWPTLFFGSHDMSRFTTRLSNGNLSKTKLJLAFL-MLTAKGIP 338

Search completed: September 20, 2005, 21:39:24
Job time : 53 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 20, 2005, 21:28:08 ; Search time 174 Seconds
(without alignments)
1012.386 Million cell updates/sec

Title: US-09-647-309A-2

Perfect score: 1822

Sequence: 1 MKAIFVLNAAPKONTWYAGG.....DRRVEIBVKGXEVVTPQQA 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1822	100.0	344	1	OMPA_KLEPN
2	1551	85.1	350	1	OMPA_ENTRAE
3	1534.5	84.2	351	1	OMPA_SHIDY
4	1520	83.4	345	1	OMPA_ECOLI
5	1520	83.4	346	2	QW821
6	1516	83.2	346	2	QPNM6
7	1514	83.1	346	2	Q9L670
8	1508	82.8	350	2	Q8Z7S0
9	1504	82.5	350	1	OMPA_SALTY
10	1496	82.1	379	2	OSCW76
11	1482	81.3	348	2	Q7UD17
12	1482	81.3	372	2	Q83RX2
13	1475	81.0	329	2	Q7X017
14	1381.5	75.8	359	1	OMPA_SERMA
15	1364	74.9	319	2	Q6QT47
16	1334.5	73.2	353	2	Q66CF0
17	1334.5	73.2	353	2	Q8ZG77
18	1334.5	73.2	363	2	Q8D056
19	1315	72.2	366	2	Q6D604
20	1294	71.0	368	2	Q7N602
21	1271.5	69.8	367	2	Q9RM69
22	1128.5	61.9	238	2	Q9N114
23	1112.5	61.1	244	2	Q47880
24	1111	61.0	243	1	OMPA_ESCFE
25	1110.5	60.9	244	2	Q9N115
26	1106	60.7	243	1	OMPA_ESCHE
27	1095.5	60.1	238	2	Q9N123
28	1089	59.8	241	1	OMPA_ESCBL
29	1056.5	58.0	238	1	OMPA_CITPR
30	1042	57.2	249	2	Q9L619
31	1012	55.5	246	2	Q9L618

32	886	48.6	243	1	OMPA_SEROD
33	849	46.6	162	2	Q6WAF8
34	843	46.3	162	2	Q6WAF6
35	843	46.3	162	2	Q6WAF7
36	843	46.3	162	2	Q6WAF9
37	835	45.8	162	2	Q6WAG0
38	835	45.8	162	2	Q6WAG1
39	835	45.8	162	2	Q6WAG2
40	835	45.8	162	2	Q6WAG3
41	835	45.8	162	2	Q6WAG4
42	737.5	40.5	163	2	Q6WAF5
43	731.5	40.1	351	2	Q6GUB7
44	731	40.1	346	2	Q51841
45	730	40.1	158	2	Q6WAH6
46	730	40.1	158	2	Q6WAH7
47	730	40.1	158	2	Q6WAH8
48	730	40.1	158	2	Q6WAH9
49	730	40.1	346	2	Q9S5J9
50	726	39.8	348	2	Q6WA10
51	725.5	39.8	353	2	Q9CMN1
52	724.5	39.8	353	2	Q6GUB4
53	720.5	39.5	161	2	Q6WAH4
54	719.5	39.5	161	2	Q6WAH0
55	717	39.4	348	2	Q6GUB6
56	716.5	39.3	353	2	Q6GUB5
57	712.5	39.1	157	2	Q6WAH1
58	712.5	39.1	157	2	Q6WAH2
59	712.5	39.1	157	2	Q6WAH3
60	712.5	39.1	157	2	Q6WAH5
61	702	38.5	348	2	Q8VPL3
62	696.5	38.2	364	2	Q6PSK1
63	696.5	38.2	364	2	Q6PSK5
64	689	37.8	344	2	Q8RML9
65	688	37.8	344	2	Q8RMM1
66	686.5	37.7	349	2	Q6GUB8
67	685	37.6	344	2	Q8RMM2
68	684	37.5	344	2	Q8RMD0
69	684	37.5	344	2	Q8RMM0
70	683	37.5	344	2	Q8RML8
71	681.5	37.4	345	2	Q6IV12
72	681.5	37.4	345	2	Q6TR54
73	680.5	37.3	341	2	Q8RJ58
74	678.5	37.2	157	2	Q6WA11
75	678.5	37.2	157	2	Q6WA15
76	674.5	37.0	157	2	Q6WA12
77	674.5	37.0	157	2	Q6WA13
78	674.5	37.0	157	2	Q6WA14
79	668.5	36.7	364	2	Q6PSU7
80	666.5	36.6	353	1	OM52_HAEIN
81	664	36.4	372	2	Q6XAY1
82	662.5	36.4	359	1	OM53_HAEIN
83	662	36.3	360	2	Q86254
84	662	36.3	378	2	Q6XAY6
85	661	36.3	372	2	Q6XAY0
86	661	36.3	372	2	Q6XAY2
87	661	36.3	378	2	Q6XAY4
88	660	36.2	374	2	Q6XAY3
89	658.5	36.1	367	2	Q6XAX4
90	657	36.1	378	2	Q9RQ28
91	655	35.9	368	2	Q65T85
92	652.5	35.8	367	2	Q6XAX6
93	650.5	35.7	367	2	Q6XAX8
94	650.5	35.7	373	2	Q6XAX9
95	647.5	35.5	162	2	Q6WAF2
96	647.5	35.5	162	2	Q6WAF4
97	646.5	35.5	353	1	OM51_HAEIN
98	646.5	35.5	367	2	Q6XAX7
99	644.5	35.4	162	2	Q6WAF3
100	630.5	34.6	360	2	Q6PSK4
101	625.5	34.3	145	2	Q93QL8
102	617	33.9	162	2	Q6WAG8
103	615	33.8	162	2	Q6WAG5
104	613.5	33.7	145	2	Q93QP3

P24755	serratia od
Q5wa18	klebsiella
Q5waf6	klebsiella
Q5waf7	klebsiella
Q5waf9	klebsiella
Q5wag0	klebsiella
Q5wag1	klebsiella
Q5wag2	klebsiella
Q5wag3	klebsiella
Q5wag4	klebsiella
Q5waf5	klebsiella
Q5gub7	pasteurella
Q51841	actinobacil
Q5wah6	enterobacte
Q5wah7	enterobacte
Q5wah8	enterobacte
Q5wah9	enterobacte
Q9S5J9	actinobacil
Q5wa10	enterobacte
Q9cmn1	pasteurella
Q5gub4	pasteurella
Q5wah4	escherichia
Q5wah0	escherichia
Q5gub6	pasteurella
Q5gub5	pasteurella
Q5wah1	escherichia
Q5wah2	escherichia
Q5wah3	escherichia
Q5wah5	escherichia
Q8VPL3	pasteurella
Q5psk1	pasteurella
Q5psk5	pasteurella
Q8rml9	haemophilus
Q8rml1	haemophilus
Q8gub8	pasteurella
Q8rmd0	haemophilus
Q8rmm2	haemophilus
Q8rml8	haemophilus
Q8rml0	haemophilus
Q6iv12	haemophilus
Q6tr54	haemophilus
Q8rj58	haemophilus
Q6wa11	citrobacter
Q6wa15	citrobacter
Q6wa12	citrobacter
Q6wa13	citrobacter
Q6wa14	citrobacter
Q6psj7	pasteurella
P38368	haemophilus
Q6xay1	pasteurella
P45996	haemophilus
Q86254	haemophilus
Q8xay6	pasteurella
Q6xay0	pasteurella
Q6xay2	pasteurella
Q6xay4	pasteurella
Q6xay3	pasteurella
Q6xax4	mannheimia
Q9RQ28	pasteurella
Q65T85	mannheimia
Q6xax6	mannheimia
Q6xax8	pasteurella
Q6xax9	pasteurella
Q6waf2	serratia pl
Q6waf4	serratia pl
P43840	haemophilus
Q6xax7	pasteurella
Q6waf3	serratia pl
Q6psk4	pasteurella
Q93QL8	erwinia car
Q6wag8	hafnia alve
Q93qp3	erwinia car

105	611	33.5	162	2	Q6WAG9	Q6Wag9	hafnia alive	178	540.5	29.7	149	2	Q93QP2	Q93qp2	erwinia rha
106	611	33.5	330	2	Q44299	Q44299	aeromonas s	179	540	29.6	146	2	Q93QO1	Q93qo1	brenneria q
107	607	33.0	162	2	Q6WAG7	Q6Wag7	hafnia alive	180	536.5	29.4	145	2	Q93QM6	Q93qm6	brenneria n
108	602	33.3	162	2	Q6WAG6	Q6Wag6	hafnia alive	181	536.5	29.4	145	2	Q93QM7	Q93qm7	brenneria n
109	601.5	33.0	149	2	Q9AQ62	Q9aq62	erwinia amy	182	536.5	29.4	145	2	Q93QM8	Q93qm8	brenneria n
110	601.5	33.0	149	2	Q9AQ64	Q9aq64	erwinia amy	183	536	29.4	146	2	Q93QM5	Q93qm5	erwinia tra
111	601.5	33.0	149	2	Q9AQ68	Q9aq68	erwinia amy	184	535.5	29.4	149	2	Q9AOS9	Q9aqs9	erwinia amy
112	601.5	33.0	149	2	Q9AQ71	Q9aq71	erwinia amy	185	534.5	29.3	149	2	Q9AQO1	Q9aqo1	erwinia tra
113	601.5	33.0	149	2	Q9AQ74	Q9aq74	erwinia amy	186	532.5	29.2	147	2	Q93QM2	Q93qm2	erwinia tra
114	601.5	33.0	149	2	Q9AQ75	Q9aq75	erwinia amy	187	532.5	29.2	147	2	Q93QM3	Q93qm3	erwinia tra
115	601.5	33.0	149	2	Q9AQ78	Q9aq78	erwinia amy	188	532.5	29.2	147	2	Q93QO6	Q93qo6	brenneria r
116	601.5	33.0	149	2	Q9AQ82	Q9aq82	erwinia amy	189	530.5	29.1	145	2	Q93QM9	Q93qm9	brenneria n
117	601.5	33.0	149	2	Q9AQ84	Q9aq84	erwinia amy	190	522	28.6	349	1	OMPA_BUCAI	P57414	buchnera ap
118	601.5	33.0	149	2	Q9AQ86	Q9aq86	erwinia amy	191	521.5	28.6	145	2	Q93QO0	Q93qo0	brenneria n
119	599.5	32.9	149	2	Q9AQ85	Q9aq85	erwinia amy	192	521	28.6	150	2	Q93QO9	Q93qo9	pectobacter
120	599.5	32.9	149	2	Q9AQ94	Q9aq94	erwinia amy	193	519.5	28.5	147	2	Q93QO9	Q93qo9	brenneria r
121	598.5	32.8	407	2	P96774	P96774	haemophilus	194	508	27.9	146	2	Q93QP9	Q93qp9	brenneria q
122	597.5	32.8	149	2	Q93QR7	Q93qr7	erwinia amy	195	507.5	27.9	147	2	Q93QO7	Q93qo7	brenneria r
123	597.5	32.8	149	2	Q9AQ83	Q9aq83	erwinia amy	196	506	27.8	146	2	Q93QO0	Q93qo0	brenneria q
124	597.5	32.8	149	2	Q9AQ80	Q9aq80	erwinia amy	197	504.5	27.7	147	2	Q93QO9	Q93qo9	brenneria r
125	597.5	32.8	149	2	Q9AQ91	Q9aq91	erwinia amy	198	502.5	27.6	147	2	Q93QO5	Q93qo5	brenneria r
126	597.5	32.8	149	2	Q9AQ92	Q9aq92	erwinia amy	199	500	27.4	146	2	Q93QO2	Q93qo2	brenneria l
127	595.5	32.7	149	2	Q9AQ56	Q9aq56	erwinia amy	200	495	27.2	146	2	Q93QO3	Q93qo3	brenneria l
128	595.5	32.7	149	2	Q9AQ57	Q9aq57	erwinia amy	201	494	27.1	146	2	Q93QP7	Q93qp7	brenneria q
129	595.5	32.7	149	2	Q9AQ58	Q9aq58	erwinia amy	202	489	26.8	148	2	Q93QO8	Q93qo8	brenneria r
130	594.5	32.6	149	2	Q93Q83	Q93qs83	erwinia amy	203	484	26.6	146	2	Q93QP8	Q93qp8	brenneria q
131	593	32.5	148	2	Q93QP1	Q93qp1	erwinia per	204	481.5	26.4	147	2	Q93QO5	Q93qo5	brenneria s
132	592.5	32.5	149	2	Q9AQ55	Q9aq55	erwinia amy	205	480.5	26.4	147	2	Q93QO1	Q93qo1	brenneria s
133	592.5	32.5	149	2	Q93QO7	Q93qo7	erwinia amy	206	480.5	26.4	147	2	Q93QO2	Q93qo2	brenneria s
134	591.5	32.5	149	2	Q93Q82	Q93qs82	erwinia amy	207	480.5	26.4	147	2	Q93QO6	Q93qo6	brenneria s
135	590.5	32.4	149	2	Q9AQ63	Q9aq63	erwinia amy	208	474.5	26.0	347	1	OMPA_BUCAP	Q8g914	buchnera ap
136	590.5	32.4	149	2	Q9AQ65	Q9aq65	erwinia amy	209	473	26.0	146	2	Q93QO4	Q93qo4	brenneria l
137	590.5	32.4	149	2	Q9AQ66	Q9aq66	erwinia amy	210	467.5	25.7	147	2	Q93QO3	Q93qo3	brenneria s
138	590.5	32.4	403	2	P96773	P96773	haemophilus	211	467.5	25.7	147	2	Q93QO4	Q93qo4	brenneria s
139	589.5	32.4	149	2	Q93Q86	Q93qs86	erwinia amy	212	464.5	25.5	149	2	Q9AQ73	Q93qo73	erwinia amy
140	589.5	32.4	149	2	Q93Q87	Q93qs87	erwinia amy	213	459	25.2	273	2	Q65T83	Q65t83	mannheimia
141	589.5	32.4	149	2	Q9AQ87	Q9aq87	erwinia amy	214	457	25.1	342	2	Q8E832	Q8e832	shewanella
142	589	32.3	344	2	Q9LA97	Q9la97	aeromonas h	215	443.5	24.3	321	2	Q31154	Q31154	vibrio chol
143	587.5	32.2	149	2	Q93QP4	Q93qp4	erwinia mal	216	416	22.8	319	2	Q87RL4	Q87rl4	vibrio para
144	585	32.1	148	2	Q93QP0	Q93qp0	pectobacter	217	387.5	21.3	324	2	Q6LJL5	Q6lj15	photobacter
145	583.5	32.0	149	2	Q93Q81	Q93qs81	erwinia amy	218	385.5	21.2	378	2	Q93IK5	Q93iks	vibrio pom
146	583.5	32.0	149	2	Q93Q84	Q93qs84	erwinia amy	219	376.5	20.7	224	2	Q62M19	Q62m19	burkholderi
147	583.5	32.0	149	2	Q93Q85	Q93qs85	erwinia amy	220	376.5	20.7	224	2	Q63R29	Q63rz9	burkholderi
148	583.5	32.0	149	2	Q93Q87	Q93qs87	erwinia amy	221	374.5	20.6	329	2	Q87GX9	Q87gx9	vibrio para
149	582.5	32.0	149	2	Q93Q85	Q93qs85	erwinia amy	222	361	19.8	231	2	Q82SL6	Q82sl6	nitrosomona
150	582.5	32.0	149	2	Q9AQ79	Q9aq79	erwinia amy	223	353	19.4	357	2	Q7MDC9	Q7mdc9	vibrio vuln
151	582.5	32.0	149	2	Q9AQ80	Q9aq80	erwinia amy	224	353	19.4	357	2	Q8D6H3	Q8d6h3	vibrio vuln
152	580.5	31.9	149	2	Q9AQ88	Q9aq88	erwinia amy	225	323	17.7	325	2	Q87JK1	Q87jki	vibrio para
153	577.5	31.7	149	2	Q93QP5	Q93qp5	erwinia mal	226	305	16.7	236	2	Q63TA5	Q63ta5	burkholderi
154	577.5	31.7	149	2	Q9AQ67	Q9aq67	erwinia amy	227	302	16.6	223	2	Q62L32	Q62l32	burkholderi
155	577	31.7	339	2	Q44298	Q44298	aeromonas s	228	286	15.7	466	2	Q74E29	Q74ez9	geobacter s
156	576.5	31.6	149	2	Q93QP6	Q93qp6	erwinia mal	229	279.5	15.3	106	2	Q9R659	Q9r659	proteus mir
157	573.5	31.5	149	2	Q9AQ93	Q9aq93	erwinia amy	230	274.5	15.1	218	2	Q8Y023	Q8y023	raistonia s
158	572.5	31.4	149	2	Q93Q80	Q93qs80	erwinia amy	231	274	15.0	193	2	Q7W527	Q7w527	bordetella
159	572.5	31.4	149	2	Q9AQ81	Q9aq81	erwinia amy	232	274	15.0	193	2	Q7WGU0	Q7wgu0	bordetella
160	571.5	31.4	149	2	Q9AQ89	Q9aq89	erwinia amy	233	271	14.9	194	1	OMPA_BORAV	Q05146	bordetella
161	571	31.3	148	2	Q93QRO	Q93qro	erwinia psi	234	266	14.6	193	2	Q7VZG6	Q7vzg6	bordetella
162	571	31.3	148	2	Q93QR2	Q93qr2	erwinia psi	235	265.5	14.6	271	2	Q62BI9	Q62bi9	burkholderi
163	570.5	31.3	149	2	Q93QR8	Q93qr8	erwinia amy	236	265.5	14.6	276	2	Q63LV3	Q63lv3	burkholderi
164	570.5	31.3	149	2	Q9AQ76	Q9aq76	erwinia amy	237	262	14.4	236	1	OMP3_NEIGO	P07050	neisseria g
165	570.5	31.3	149	2	Q9AQ77	Q9aq77	erwinia amy	238	256	14.1	365	2	Q8PC19	Q8pc19	xanthomonas
166	563.5	30.9	149	2	Q9AQ69	Q9aq69	erwinia amy	239	256	14.1	365	2	Q8PNP2	Q8pnp2	xanthomonas
167	562.5	30.9	145	2	Q93QN7	Q93qn7	brenneria a	240	254	13.9	317	2	Q51777	Q51777	pseudomonas
168	559.5	30.7	149	2	Q93QR3	Q93qr3	erwinia psi	241	253	13.9	321	2	Q9WW15	Q9ww15	pseudomonas
169	558.5	30.7	149	2	Q93QR9	Q93qr9	erwinia amy	242	253	13.9	326	2	Q9S4R5	Q9s4r5	pseudomonas
170	557.5	30.6	149	2	Q9AQ61	Q9aq61	erwinia amy	243	252.5	13.9	296	2	Q6VQV3	Q6vqv3	pseudomonas
171	555.5	30.5	147	2	Q93QN8	Q93qn8	erwinia chr	244	252	13.8	264	2	Q88NT2	Q88nt2	pseudomonas
172	555.5	30.5	149	2	Q93QRA	Q93qra	erwinia psi	245	251	13.8	317	2	Q51780	Q51780	pseudomonas
173	555.5	30.5	149	2	Q9AQ60	Q9aq60	erwinia amy	246	250	13.7	242	1	OMP4_NEIMA	P38367	neisseria m
174	548.5	30.1	149	2	Q93QMO	Q93qmo	erwinia tra	247	249.5	13.7	370	2	Q8EBH3	Q8ebh3	shewanella
175	548.5	30.1	149	2	Q93QMA	Q93qma	erwinia tra	248	249	13.7	317	2	Q51721	Q51721	pseudomonas
176	547.5	30.0	149	2	Q9AQ72	Q9aq72	erwinia amy	249	248	13.6	317	2	Q51781	Q51781	pseudomonas
177	546	30.0	148	2	Q93QR1	Q93qr1	erwinia psi	250	248	13.6	356	2	Q6RYW5	Q6ryw5	acinetobact

251 247.5 13.6 322 2 Q9X4R6
 252 247.5 13.6 325 2 Q9X4R8
 253 247 13.6 831 2 Q88IA9
 254 246.5 13.5 325 2 Q9X4R7
 255 246 13.5 326 2 Q9X4S0
 256 244 13.4 299 2 Q63UE6
 257 243.5 13.4 326 1 PORF_PSEFL
 258 243 13.3 317 2 Q51778
 259 242.5 13.3 429 2 Q74G87
 260 242 13.3 272 2 Q6VQT8
 261 241.5 13.3 298 2 Q6VQV8
 262 241.5 13.3 298 2 Q52465
 263 240 13.2 317 2 Q52465
 264 237 13.0 297 2 Q6VQU2
 265 233 12.8 226 2 Q7NS55
 266 232.5 12.8 281 2 Q6PBS5
 267 231.5 12.7 350 1 PORF_PSEAB
 268 230 12.6 318 2 Q9X4S1
 269 229.5 12.6 272 2 Q65TF8
 270 228 12.5 152 2 Q9S3M1
 271 227.5 12.5 407 2 Q9AA59
 272 227 12.5 297 2 Q6VQW2
 273 226 12.4 319 2 Q6LND3
 274 226 12.4 368 2 Q9LAJ4
 275 225 12.3 297 2 Q6VQU3
 276 225 12.3 346 2 Q8KWW6
 277 225 12.3 355 2 Q6FE98
 278 222.5 12.2 296 2 Q51779
 279 222.5 12.2 321 2 Q9XCZ3
 280 222.5 12.2 321 2 Q9XCZ6
 281 221 12.1 317 2 Q6VQW1
 282 220 12.1 328 2 Q9XCZ7
 283 219 12.0 344 2 Q9X4S3
 284 218 12.0 344 2 Q883Q1
 285 215 11.8 284 2 Q85277
 286 213.5 11.7 343 2 Q9XCZ4
 287 212.5 11.7 343 2 Q9S6B8
 288 212 11.6 346 2 Q9X4R9
 289 211 11.6 340 2 Q9X4S2
 290 210 11.5 273 2 Q84292
 291 210 11.5 322 2 Q6VQV6
 292 210 11.5 323 2 Q9XCZ5
 293 210 11.5 344 2 Q88L46
 294 209.5 11.5 318 2 Q6VQV9
 295 209 11.5 214 2 Q6MJK7
 296 209 11.5 287 2 Q9X4B1
 297 209 11.5 344 2 Q9X4L6
 298 208.5 11.4 319 2 Q9PMI4
 299 207.5 11.4 318 2 Q6VQV9
 300 207.5 11.4 318 2 Q6VQW0

ALIGNMENTS

RESULT 1
 OMPA_KLEPN
 ID OMPA_KLEPN STANDARD; PRT; 344 AA.
 AC P24017; O69435; PRT;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Outer membrane protein A precursor (Outer membrane protein II).
 GN Name=ompA;
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RV 308;
 RX MEDLINE=98192544; PubMed=9524233; DOI=10.1016/S0378-1119(98)00060-2;
 RA Nguyen T.N., Samuelson P., Sterky F., Merle-Poitte C., Robert A.,

BAUSSANT T., Haeuw J.F., Uhlen M., Binz H., Stahl S.;
 "Chromosomal sequencing using a PCR-based biotin-capture method
 allowed isolation of the complete gene for the outer membrane protein
 A of Klebsiella pneumoniae.";
 Gene 210:93-101(1998).
 [2]
 SEQUENCE OF 93-335 FROM N.A.
 STRAIN=LD119;
 MEDLINE=92065252; PubMed=1955870;
 LAWRENCE J.G., Ochman H., Hartl D.L.;
 "Molecular and evolutionary relationships among enteric bacteria.";
 J. Gen. Microbiol. 137:1911-1921(1991).
 -!- FUNCTION: Required for the action of colicins K and L and for the
 stabilization of mating aggregates in conjugation. Serves as a
 receptor for a number of T-even like phages. Also acts as a porin
 with low permeability that allows slow penetration of small
 solutes (By similarity).
 -!- SUBUNIT: Monomer (Probable).
 -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
 -!- SIMILARITY: Belongs to the ompA family.

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 EMBL; AJ000998; CAA04450.1; -;
 EMBL; M63355; AAA25119.1; -;
 HSSP; P02934; 1QJP.
 InterPro; IPR006664; Bac_OmpA.
 InterPro; IPR002368; OmpA.
 InterPro; IPR006665; OmpA/MotB.
 InterPro; IPR006690; OmpA_LIKE.
 InterPro; IPR000498; OmpA_tmem.
 Pfam; PF00691; OmpA; 1.
 Pfam; PF01389; OmpA membrane; 1.
 PRINTS; PR01021; OMPADOMAIN.
 PRODOM; PD000930; OmpA; 1.
 PROSITE; PS01068; OmpA; 1.
 Conjugation; Outer membrane; Phage recognition; Porin; Repeat; Signal;
 Transmembrane.
 SIGNAL 1 ? Potential.
 CHAIN 1 ? 344 Outer membrane protein A.
 TRANSMEM 15 28 Potential.
 TRANSMEM 48 60 Potential.
 TRANSMEM 63 78 Potential.
 TRANSMEM 90 100 Potential.
 TRANSMEM 104 119 Potential.
 TRANSMEM 140 151 Potential.
 TRANSMEM 157 173 Potential.
 TRANSMEM 179 190 Potential.
 DOMAIN 199 206 4 X 2 AA tandem repeats of A-P.
 REPEAT 199 200 1.
 REPEAT 201 202 2.
 REPEAT 203 204 3.
 REPEAT 205 206 4.
 DOMAIN 255 299 OmpA-like.
 DISULFID 309 321 By similarity.
 CONFLICT 335 335 Y -> I (in Ref. 2).
 SQ SEQUENCE 344 AA; 37061 MW; AC88AAE3B7871B16 CRC64;
 Query Match 100.0%; Score 1822; DB 1; Length 344;
 Best Local Similarity 100.0%; Pred. No. 7.7e-132; Indels 0; Gaps 0;
 Matches 344; Conservative 0; Mismatches 0;
 QY 1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGYGNGFONNNGPTRNDOLGAGAFGGYQVN 60
 |||||
 DB 1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGYGNGFONNNGPTRNDOLGAGAFGGYQVN 60
 |||||
 QY 61 PYLGFMGYDGLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMVWRADS 120

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Db 61 PYLGFEMCYDMLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADS 120
Qy 121 KGNVASTGVSRSEHDTGVSVPFAGGVEWAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGM 180
Db 121 KGNVASTGVSRSEHDTGVSVPFAGGVEWAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGM 180
Qy 181 LSLGVSYRFGQEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 240
Db 181 LSLGVSYRFGQEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 240
Qy 241 TQLSNMDFKDSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPACKISARGMGE 300
Db 241 TQLSNMDFKDSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPACKISARGMGE 300
Qy 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPOA 344
Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPOA 344
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RESULT 2

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OMPA_ENTAE STANDARD; PRT; 350 AA.
AC P09146;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Outer membrane protein A precursor.
GN Name=ompA;
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=548;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84108348; PubMed=6363059;
RA Braun G., Cole S.T.;
RT "Molecular characterization of the gene coding for major outer
  membrane protein OmpA from Enterobacter aerogenes.";
RL Eur. J. Biochem. 137:495-500(1983).
CC -!- FUNCTION: Required for the action of colicins K and L and for the
  stabilization of mating aggregates in conjugation. Serves as a
  receptor for a number of T-even like phages. Also acts as a porin
  with low permeability that allows slow penetration of small
  solutes (By similarity).
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -!- SIMILARITY: Belongs to the ompA family.
-----
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DR EMBL; X00254; CAA25062.1; -.
DR F01; S07222; S07222.
DR HSSP; P02934; 1QJP.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/NotB.
DR InterPro; IPR006690; OmpA_LIKE.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01389; OmpA_membrane; 1.
DR PROSITE; PR01021; OMPADOMAIN.
DR ProDom; PD000930; OmpA/NotB; 1.
DR PROSITE; PS01068; OmpA; 1.
KW Conjugation; Outer membrane; Phage recognition; Porin; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 21
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FT CHAIN 22 350 Outer membrane protein A.
FT TRANSMEM 27 40 Potential.
FT TRANSMEM 59 71 Potential.
FT TRANSMEM 74 89 Potential.
FT TRANSMEM 101 111 Potential.
FT TRANSMEM 115 130 Potential.
FT TRANSMEM 146 157 Potential.
FT TRANSMEM 163 179 Potential.
FT TRANSMEM 185 196 Potential.
FT DOMAIN 205 212 4 X 2 AA tandem repeats of A-P.
FT REPEAT 207 208 1.
FT REPEAT 209 210 2.
FT REPEAT 211 212 3.
FT DOMAIN 261 305 OmpA-like.
FT DISULFID 315 327 By similarity.
SQ SEQUENCE 350 AA; 37575 MW; 6276C6F2F21065DA CRC64;

Query Match 85.1%; Score 1551; DB 1; Length 350;
Best Local Similarity 87.6%; Pred. No. 5.4e-111;
Matches 297; Conservative 10; Mismatches 26; Indels 6; Gaps 2;

Qy 6 VLNAAPKDNWTYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGQYQNPYLGP 65
Db 18 VAQAAPKDNWTYAGGKLGWSQYHDTGWY-NSNLNNGPTHESQLGAGAFGQYQNPYLGF 76
Qy 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
Db 77 EMGYDWLGRMPYKGVKNGVAFSSQAVQLTAKLGYPITDDLDIYTRLGGMVWRADS----- 131
Qy 126 STGVSRSEHDTGVSVPFAGGVEWAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
Db 132 SNSIAGDNHDTGVSVPFAGGVEWAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGV 191
Qy 186 SYRFGQEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 245
Db 192 SYRFGQEDNAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 251
Qy 246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPACKISARGMGESNPVT 305
Db 252 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPACKISARGMGESNPVT 311
Qy 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPOA 344
Db 312 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPOA 350

RESULT 3
OMPA_SHIDY STANDARD; PRT; 351 AA.
AC P02935;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Outer membrane protein A precursor (Outer membrane protein II).
GN Name=ompA;
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=622;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82221414; PubMed=6283478;
RA Braun G., Cole S.T.;
RT "The nucleotide sequence coding for major outer membrane protein OmpA
  of Shigella dysenteriae.";
RL Nucleic Acids Res. 10:2367-2378(1982).
CC -!- FUNCTION: Required for the action of colicins K and L and for the
  stabilization of mating aggregates in conjugation. Serves as a
  receptor for a number of T-even like phages. Also acts as a porin
  with low permeability that allows slow penetration of small
  solutes (By similarity).
CC -!- SUBUNIT: Monomer (Probable).
```

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CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC CC -!- SIMILARITY: Belongs to the ompA family.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: V01344; CAA24638.1; -.
CC CC PIR: A03435; MNEBAD.
CC CC HSP: P02934; IQJP.
CC CC InterPro: IPR006664; Bac OmpA.
CC CC InterPro: IPR002368; OmpA.
CC CC InterPro: IPR006665; OmpA/MotB.
CC CC InterPro: IPR006690; OMPA-LIKE.
CC CC InterPro: IPR000498; OmpA_Cmem.
CC CC Pfam: PF00691; OmpA; 1.
CC CC Pfam: PF01389; OmpA_membrane; 1.
CC CC PRINTS: PR01021; OMPADOMAIN.
CC CC ProDom: PD000930; OmpA/MotB; 1.
CC CC PROSITE: PS01068; OMPA; 1.
CC CC Conjugation; Outer membrane; Phage recognition; Porin; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 21
FT CHAIN 22 351 Outer membrane protein A.
FT TRANSMEM 27 40 Potential.
FT TRANSMEM 55 67 Potential.
FT TRANSMEM 70 85 Potential.
FT TRANSMEM 97 107 Potential.
FT TRANSMEM 111 126 Potential.
FT TRANSMEM 147 158 Potential.
FT TRANSMEM 164 180 Potential.
FT TRANSMEM 186 197 Potential.
FT DOMAIN 206 213 4 X 2 AA tandem repeats of A-P.
FT REPEAT 206 207 1.
FT REPEAT 208 209 2.
FT REPEAT 210 211 3.
FT REPEAT 212 213 4.
FT REPEAT 212 213 4.
FT DOMAIN 262 306 OmpA-like.
FT DISULFID 316 328 By similarity.
FT SEQUENCE 351 AA; 37741 MW; 1499AA5F5395B35B CRC64;

Query Match 84.2%; Score 1534.5; DB 1; Length 351;
Best Local Similarity 84.7%; Pred. No. 1e-109;
Matches 287; Conservative 20; Mismatches 27; Indels 5; Gaps 1;

Qy 6 VLNAAPKDNWTYAGKLGWSQYHDTGTFYGNQFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
Db 18 VAQAAPKDNWTYTGAKLGWSQYHDTGTFI-----DNNNGPTHEQLGAGAFGGYQVNPYGF 72

Qy 66 EMGYDNLGRMAYKGSVDNAGPAQGVQLTAKLGYPTDLDIYTRLGGWVRADSKGNYA 125
Db 73 EMGYDNLGRMPYKGSVENGAYKAQGVQLTAKLGYPTDLDIYTRLGGWVRADTKAHN 132

Qy 126 STGVSRSHDTGVSVPFAGGVWAVTRDIATRLFYQWNNIGDAGTVCTRPDNGMLSLGV 185
Db 133 VTGSEKNHDTGVSVPFAGGVWAVTPEIATRLFYQWNNIGDAGTVCTRPDNGMLSLGV 192

Qy 186 SYRFGQEDAAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 245
Db 193 SYRFGQGEAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 252

Qy 246 MDPKDGSAVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
Db 253 LDPKDGSAVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 312

Qy 306 GNTCDNVKARALIDCLAPDRRVEIKYKVVVTPQQA 344
Db 313 GNTCDNVKQRAALIDCLAPDRRVEIKYKVVVTPQQA 351

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RESULT 4
OMPA_ECOLI STANDARD; PRT; 346 AA.
ID P02934;
DC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Outer membrane protein A precursor (Outer membrane protein II*).
GN Name=ompA; Synonyms=con, tolG, tut;
GN OrderedLocusName=B0957, z1307, ECs1041;
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=81053729; PubMed=6253901;
RA Beck E., Bremer E.;
RT "Nucleotide sequence of the gene ompA coding the outer membrane
RT protein II of Escherichia coli K-12.";
RL Nucleic Acids Res. 8:3011-3024 (1980).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=81170587; PubMed=6260961;
RA Movva N.R., Nakamura K., Inouye M.;
RT "Gene structure of the OmpA protein, a major surface protein of
RT Escherichia coli required for cell-cell interaction.";
RL J. Mol. Biol. 143:317-328 (1980).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155 (1996).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533 (2001).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

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RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
RL O157:H7 and genomic comparison with a laboratory strain K-12."; [7]
RN DNA Res. 8:11-22(2001).
RP SEQUENCE OF 22-346.
RC STRAIN=K12;
RX MEDLINE=81054820; PubMed=7001461;
RA Chen R., Schmidmayr W., Kramer C., Chen-Schmeisser U., Henning U.;
RT "Primary structure of major outer membrane protein II (OmpA protein)
RL of *Escherichia coli* K-12."; [7]
RN Proc. Natl. Acad. Sci. U.S.A. 77:4592-4596(1980).
RP SEQUENCE OF 22-32.
RC STRAIN=K12 / W3110;
RA Pasquali C., Sanchez J.-C., Ravier F., Golaz O., Hughes G.J.,
RT Frutiger S., Paquet N., Wilkins M., Appel R.D., Bairoch A.,
RL Hochstrasser D.F.;
RN Submitted (SEP-1994) to Swiss-Prot.
RP SEQUENCE OF 22-34.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RL in the genome of *Escherichia coli* K-12."; [10]
RN Electrophoresis 18:1259-1313(1997).
RP SEQUENCE OF 22-26.
RC STRAIN=K12 / W3110;
RX MEDLINE=98291876; PubMed=9629924;
RA Molloy M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traini M.,
RT Sanchez J.-C., Hochstrasser D.F., Williams K.L., Gooley A.A.;
RL "Extraction of membrane proteins by differential solubilization for
RL separation using two-dimensional gel electrophoresis."; [11]
RN Electrophoresis 19:837-844(1998).
RP MUTANTS RESISTANT TO PHAGE ENTRY.
RX MEDLINE=84264337; PubMed=6086577;
RA Morona R., Klose M., Henning U.;
RT "*Escherichia coli* K-12 outer membrane protein (OmpA) as a
RL bacteriophage receptor: analysis of mutant genes expressing altered
RL proteins."; [12]
RN J. Bacteriol. 159:570-578(1984).
RP MUTANTS RESISTANT TO PHAGE ENTRY.
RX MEDLINE=86033606; PubMed=3902787;
RA Morona R., Kramer C., Henning U.;
RT "Bacteriophage receptor area of outer membrane protein OmpA of
RL *Escherichia coli* K-12."; [13]
RN J. Bacteriol. 164:539-543(1985).
RP PORIN ACTIVITY.
RC STRAIN=K12;
RX MEDLINE=92129334; PubMed=1370823;
RA Sugawara E., Nikaido H.;
RT "Pore-forming activity of OmpA protein of *Escherichia coli*."; [14]
RN J. Biol. Chem. 267:2507-2511(1992).
RP SUBCELLULAR LOCATION.
RX PubMed=7813480;
RA Kuhn A., Kiefer D., Koehne C., Zhu H.-Y., Tschantz W.R., Dalbey R.E.;
RT "Evidence for a loop-like insertion mechanism of pro-Omp A into the
RL inner membrane of *Escherichia coli*."; [15]
RN Eur. J. Biochem. 226:891-897(1994).
RP TOPOLOGY.
RX MEDLINE=94148615; PubMed=8106193;
RA Gromiha M.M., Ponnuswamy P.K.;
RT "Prediction of transmembrane beta-strands from hydrophobic
RL characteristics of proteins."; [15]
RN Int. J. Pept. Protein Res. 42:420-431(1993).

RN [16]
RP TOPOLOGY.
RX MEDLINE=99296577; PubMed=10368142;
RA Koebnik R.;
RT "Structural and functional roles of the surface-exposed loops of the
RL beta-barrel membrane protein OmpA from *Escherichia coli*."; [7]
RN J. Bacteriol. 181:3688-3694(1999).
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 22-192.
RX MEDLINE=99023200; PubMed=9808047;
RA Pautsch A., Schulz G.E.;
RT "Structure of the outer membrane protein A transmembrane domain."; [8]
RN Nat. Struct. Biol. 5:1013-1017(1998).
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
RX MEDLINE=20229895; PubMed=10764596; DOI=10.1006/jmbi.2000.3671;
RA Pautsch A., Schulz G.E.;
RT "High-resolution structure of the OmpA membrane domain."; [9]
RN J. Mol. Biol. 298:273-282(2000).
RP STRUCTURE BY NMR OF 22-197.
RX PubMed=11276254; DOI=10.1038/86214;
RA Arora A., Abildgaard F., Bushweller J.H., Tamm L.K.;
RT "Structure of outer membrane protein A transmembrane domain by NMR
RL spectroscopy."; [20]
RN Nat. Struct. Biol. 8:334-338(2001).
RP MASS SPECTROMETRY.
RX MEDLINE=20222957; PubMed=10757971; DOI=10.1021/bi000150m;
RA le Coutre J., Whitelegge J.P., Gross A., Turk E., Wright E.M.,
RL Kaback H.R., Faull K.F.;
RT "Proteomics on full-length membrane proteins using mass
RL spectrometry."; [19]
RN Biochemistry 39:4237-4242(2000).
CC -!- FUNCTION: Required for the action of colicins K and L and for the
CC stabilization of mating aggregates in conjugation. Serves as a
CC receptor for a number of T-even like phages. Also acts as a porin
CC with low permeability that allows slow penetration of small
CC solutes.
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -!- MASS SPECTROMETRY: MW=35177; METHOD=Electrospray; RANGE=22-346;
CC NOTE=Ref.20.
CC -!- SIMILARITY: Belongs to the ompA family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; V00307; CAA23588.1; -;
CC EMBL; U00096; AAC74043.1; -;
CC EMBL; D90733; BAA35715.1; -;
CC EMBL; D90734; BAA35722.1; -;
CC -----
CC Query Match 83.4%; Score 1520; DB 1; Length 346;
CC Best Local Similarity 85.0%; Pred. No. 1.3e-108;
CC Matches 288; Conservative 17; Mismatches 24; Indels 10; Gaps 2;
Qy 6 VLNAAPKNDTWYAGGKLGWSQYHDTGVGVGFGFNNNGPTRNDOLGAGAFGQVNPVYGF 65
Db 18 VAQAAPKNDTWYTGAKLGWSQYHDTGFI-----NNGGPTHEHQLGAGAFGQVNPVYGF 72
Qy 66 EMGYDVLGRMAYKGSVDNGAFKAGVQLTAKLGYPITDDLDIYTRLGGMWRADSKGNYA 125
Db 73 EMGYDVLGRMPYKGSVENGAYKAGVQLTAKLGYPITDDLDIYTRLGGMWRADTKSN-- 130
Qy 126 STGVSRSEHDTGVSPFAGGVEMAVTRDIAIATRLRYQVNNIGDAGTVGTRPDNGMLSLGV 185
Db 131 ---VYGNKNDTGVSPFAGGVEMAVTRDIAIATRLRYQVNNIGDAGTVGTRPDNGMLSLGV 187

	Query Match	83.2%;	Score 1516;	DB 2;	Length 346;
	Best Local Similarity	84.7%;	Pred. No. 2.6e-108;		
	Matches 287;	Conservative 17;	Mismatches 25;	Indels 10;	Gaps 2
Qy	6	VLNAAPKDNTWYAGGKLGWSYHDTGFGVNGFQNNNGTRNDOLGAGAGGGVQVNPYGLG	65		
Db	18	VAQAAPKDNTWYTGAKLGWSYHDTGFI-----NNNGPTHEQLGAGAGGGVQVNPYVGF	72		
Qy	66	EMGYDMLGRMAYKGSVDNGAFKAGQVQLTAKLGYPIITDDLDIYTRLGGVMWRADSKGNYA	125		
Db	73	EMGYDMLGRMPYKGSVNGAYKAQGVQLTAKLGYPIITDDLDIYTRLGGVMWRADTKSN--	130		
Qy	126	STGVSRSEHDTGSPVFAGGVGEWAVTRDIAIRLEYQWVNNITGDAGTVGTRPDNGMLSLGV	185		
Db	131	---VYGNKHDTGSPVFAGGVGEYAITETIAIRLEYQWNTNITGDAITIGTRPDNGMLSLGV	187		


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Qy 186 SYRFGQDAAPVAPAPAPAEVATKFTLKSVDLFFNFKNATLKPGEQOALDQLYTOLSN 245
Db 188 SYRFGQGEAAPVAPAPAPAEVQTKFTLKSVDLFFNFKNATLKPGEQOALDQLYSOLSN 247
Qy 246 MDPKDGSAVLGYTDRIQSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
Db 248 LDPKDGSAVLGYTDRIQSDAYNQOLSERRAQSVVDYLVAKGIPVDKISARGMGESNPVT 307
Qy 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPOA 344
Db 308 GNTCDNVKQRAALIDCLAPDRRVEIEVKIGIKDVVTQPOA 346

RESULT 7
Q9L6J0 PRELIMINARY; PRT; 346 AA.
AC Q9L6J0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein A.
GN Name=ompA;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=RS218;
RA Wang Y., Kim K.S.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ompA family.
DR EMBL; AF234269; AAF37887.1; -.
DR HSSP; P02934; 1QJP.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR006664; Bac OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR006690; OmpA LIKE.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMEMBRANE.
DR ProDom; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OMPA; 1.
SQ SEQUENCE 346 AA; 37188 MW; 5736077E41B84C3 CRC64;

Query Match 83.1%; Score 1514; DB 2; Length 346;
Best Local Similarity 84.4%; Pred. No. 3.7e-108;
Matches 286; Conservative 18; Mismatches 25; Indels 10; Gaps 2;

Qy 6 VLNAAPKDNWTYAGKLGWSQYHDTGFGYNGFGNNQGNPTNDQLGAGAFGQYQNPYLGF 65
Db 18 VAQAAPKDNWTYAGKLGWSQYHDTGFI-----NNGGPTHENQLGAGAFGQYQNPYVGF 72
Qy 66 EMGYDWMGRMAYKGSVDNGAFKAQGVOLTKAGLYPIITDDLDIYTRLGGMVWRADSKGNYA 125
Db 73 EMGYDWMGRMPYKGSVENGAYKAQGVOLTKAGLYPIITDDLDVYTRLGGMVWRADTKSN-- 130
Qy 126 STGVSRSEHDTGVSFVAGGVEWAVTRDIATRLLEYQWNNIGDAGTVTRPDNGMLSLGV 185
Db 131 ---VYGNKHNDTGVSPFAGGVEYAITPEIATRLLEYQWNTNNGIDARTIGTRPDNGMLSLGV 187
Qy 186 SYRFGQDAAPVAPAPAPAEVATKFTLKSVDLFFNFKNATLKPGEQOALDQLYTOLSN 245
Db 188 SYRFGQGEAAPVAPAPAPAEVQTKFTLKSVDLFFNFKNATLKPGEQOALDQLYSOLSN 247
Qy 246 MDPKDGSAVLGYTDRIQSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
Db 248 LDPKDGSAVLGYTDRIQSDAYNQALSERRAQSVVDYLVAKGIPADKISARGMGESNPVT 307
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Qy 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPOA 344
Db 308 GNTCDNVKQRAALIDCLAPDRRVEIEVKIGIKDVVTQPOA 346

RESULT 8
Q8Z7S0 PRELIMINARY; PRT; 350 AA.
AC Q8Z7S0; Q7C962;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Outer membrane protein A.
GN Name=ompA; OrderedLocNames=STY1091, t1850;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jørgels K.,
RA Quig A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -1- SIMILARITY: Belongs to the ompA family.
DR EMBL; AL627269; CAD08196.1; -.
DR EMBL; AE016840; AA069468.1; -.
DR HSSP; P02934; 1QJP.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; GO:0005198; F: structural molecule activity; IEA.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMEMBRANE.
DR ProDom; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OMPA; 1.
DR Complete proteome.
SQ SEQUENCE 350 AA; 37477 MW; EEB90059DFCADFD3 CRC64;

Query Match 82.8%; Score 1508; DB 2; Length 350;
Best Local Similarity 82.9%; Pred. No. 1.1e-107;
Matches 281; Conservative 26; Mismatches 26; Indels 6; Gaps 2;

Qy 6 VLNAAPKDNWTYAGKLGWSQYHDTGFGYNGFGNNQGNPTNDQLGAGAFGQYQNPYLGF 65
Db 18 VAQAAPKDNWTYAGKLGWSQYHDTGFI-----HNDGPTHENQLGAGAFGQYQNPYVGF 72
Qy 66 EMGYDWMGRMAYKGSVDNGAFKAQGVOLTKAGLYPIITDDLDIYTRLGGMVWRADSKGNYA 125
Db 73 EMGYDWMGRMPYKGSVDNTNGAYKAQGVOLTKAGLYPIITDDLDVYTRLGGMVWRADTKSNP 132
Qy 126 STGVSRSEHDTGVSFVAGGVEWAVTRDIATRLLEYQWNNIGDAGTVTRPDNGMLSLGV 185
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[1]
RN  SEQUENCE FROM N.A.
RP  STRAIN=06:H1 / CT073 / ATCC 700928 / UPEC;
RX  MEDLINE=2238234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA  Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA  RasKO D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA  Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA  Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT  "Extensive mosaic structure revealed for the complete genome sequence
RT  of uropathogenic Escherichia coli.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
CC  -!- SIMILARITY: Belongs to the ompA family.
DR  EMBL; AE016758; AAN79561.1; -.
DR  HSSP; P02934; 1QJP.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR  GO; GO:0005198; F:structural molecule activity; IEA.
DR  InterPro; IPR006664; Bac OmpA.
DR  InterPro; IPR002368; OmpA.
DR  InterPro; IPR006665; OmpA/MotB.
DR  InterPro; IPR006690; OmpA LIKE.
DR  Pfam; PF00691; OmpA; 1.
DR  Pfam; PF01389; OmpA membrane; 1.
DR  PRINTS; PR01021; OMPADOMAIN.
DR  PRINTS; PR01022; OUTERMEMBRANE.
DR  PRODOM; PD000930; OmpA/MotB; 1.
DR  PROSITE; PS01068; OmpA; 1.
KW  Complete proteome.
SQ  SEQUENCE 379 AA; 41054 MW; CE396D152EB1EDCA CRC64;

Query Match      82.1%; Score 1496; DB 2; Length 379;
Best Local Similarity 83.8%; Pred. No. 1e-106;
Matches 284; Conservative 17; Mismatches 32; Indels 6; Gaps 2;

Qy  6  VLNAAPKDNWTWYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
Db  47  VAQAPKDNWTWYTGAKLGWSQYHDTGFI-----PNNGPTHEQLGAGAFGGYQVNPYGVF 101
Qy  66  EMGYDNLGRMAYKGSVDNGAFKAQGVQLTAKLGVPITDDLDIYTRLCGMVWRADSKGNYA 125
Db  102  EMGYDNLGRMPYKGDNINGAYKAQGVQLTAKLGVPITDDLDIYTRLCGMVWRADTKANVP 161
Qy  126  STGVSRSRSHDTGVSFVAGGVEMAVTRDIATRELYQWNNIGDAGTGTTRPDNGMLSLGV 185
Db  162  G-GASFQKHDDTGVSPFAGGVETAITPEIATRELYQWNTNIGDAHTIGTRPDNGMLSLGV 220
Qy  186  SYRFGQEDAAVPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 245
Db  221  SYRFGQGEVAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 280
Qy  246  MDPKDGSAVLGYTDTRIGSEAYNQSLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
Db  281  LDPKDGSAVLGYTDTRIGSDAYNQALSERRAQSVVDYLVAKGIPADKISARGMGESNPVT 340
Qy  306  GNTCDNVKARAALIDCLAPDRRVEIEVKGVEVVTQPOA 344
Db  341  GNTCDNVKQRAALIDCLAPDRRVEIEVKGIDVVTQPOA 379

RESULT 11
Q7UD17 ID Q7UD17 PRELIMINARY; PRT; 348 AA.
AC Q7UD17;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein 3a (II*G;d).
GN Name=ompA; OrderedLocusNames=S1023;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;

[1]
RN  SEQUENCE FROM N.A.
RP  STRAIN=24577;
RX  MEDLINE=22590274; PubMed=12704152;
RA  Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA  Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA  Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA  Schwartz D.C., Blattner F.R.;
RT  "Complete genome sequence and comparative genomics of Shigella
RT  flexneri serotype 2a strain 2457T.";
RL  Infect. Immun. 71:2775-2786 (2003).
DR  EMBL; AE016981; AAP16471.1; -.
DR  HSSP; P02934; 1BXW.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR  InterPro; IPR006665; OmpA/MotB.
DR  InterPro; IPR006690; OmpA LIKE.
DR  InterPro; IPR000498; OmpA_tmem.
DR  Pfam; PF00691; OmpA; 1.
DR  Pfam; PF01389; OmpA membrane; 1.
DR  PRODOM; PD000930; OmpA/MotB; 1.
DR  PROSITE; PS01068; OmpA; 1.
SQ  SEQUENCE 348 AA; 37283 MW; 42623C67041D62F4 CRC64;

Query Match      81.3%; Score 1482; DB 2; Length 348;
Best Local Similarity 83.5%; Pred. No. 1.1e-105;
Matches 283; Conservative 18; Mismatches 30; Indels 8; Gaps 3;

Qy  6  VLNAAPKDNWTWYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
Db  18  VAQAPKDNWTWYTGAKLGWSQYHDTGFI-----PNNGPTHEQLGAGAFGGYQVNPYGVF 72
Qy  66  EMGYDNLGRMAYKGSVDNGAFKAQGVQLTAKLGVPITDDLDIYTRLCGMVWRADSKGNYA 125
Db  73  EMGYDNLGRMPYKGDNINGAYKAQGVQLTAKLGVPITDDLDIYTRLCGMVWRADTKANVP 132
Qy  126  STGVSRSRSHDTGVSFVAGGVEMAVTRDIATRELYQWNNIGDAGTGTTRPDNGMLSLGV 185
Db  133  G-GASFQKHDDTGVSPFAGGVETAITPEIATRELYQWNTNIGDAHTIGTRPDNGMLSLGV 191
Qy  186  SYRFGQEDAAVPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 245
Db  192  SYRFGQGEAPV--APAPAPVQTKHTLKSVDLVLFNFNKAATLKPEGQALDQLYSQLN 249
Qy  246  MDPKDGSAVLGYTDTRIGSEAYNQSLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
Db  250  LDPKDGSAVLGYTDTRIGSDAYNQALSERRAQSVVDYLVAKGIPADKISARGMGESNPVT 309
Qy  306  GNTCDNVKARAALIDCLAPDRRVEIEVKGVEVVTQPOA 344
Db  310  GNTCDNVKQRAALIDCLAPDRRVEIEVKGIDVVTQPOA 348

RESULT 12
Q83RX2 ID Q83RX2 PRELIMINARY; PRT; 372 AA.
AC Q83RX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein A.
GN Name=ompA; OrderedLocusNames=SF0957;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN  SEQUENCE FROM N.A.
RP  STRAIN=301 / Serotype 2a;
RX  MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA  Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA  Yang J., Yang F., Zhang X., Zhang J., Zhang J., Wu H., Qu D., Dong J.,
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RT protein.";
RL Mol. Gen. Genet. 195:321-328(1984).
CC -!- FUNCTION: Required for the action of colicins K and L and for the
CC stabilization of mating aggregates in conjugation. Serves as a
CC receptor for a number of T-even like phages. Also acts as a porin
CC with low permeability that allows slow penetration of small
CC solutes (by similarity).
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -!- SIMILARITY: Belongs to the ompA family.
CC -----
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CC entities requires a license agreement. Usage by and for commercial
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X00618; CRA25254.1; -.
CC F1R; S07298; S07298.
CC HSSP; P02934; IQJP.
CC InterPro; IPR006664; Bac_OmpA.
CC InterPro; IPR002368; OmpA.
CC InterPro; IPR006665; OmpA/MotB.
CC InterPro; IPR006690; OMPA LIKE.
CC InterPro; IPR000498; OmpA_tmem.
CC Pfam; PF00691; OmpA; 1.
CC Pfam; PF01389; OmpA membrane; 1.
CC PRINTS; PR01021; OMPADOMAIN.
CC ProDom; PD000930; OmpA/MotB; 1.
CC PROSITE; PS01068; OmpA; 1.
CC Conjugation; Outer membrane; Phage recognition; Porin; Repeat; Signal;
CC Transmembrane.
KW SIGNAL 1 21
FT CHAIN 22 359 Outer membrane protein A.
FT TRANSMEM 27 40 Potential.
FT TRANSMEM 62 74 Potential.
FT TRANSMEM 77 92 Potential.
FT TRANSMEM 104 114 Potential.
FT TRANSMEM 118 133 Potential.
FT TRANSMEM 154 165 Potential.
FT TRANSMEM 171 187 Potential.
FT TRANSMEM 193 204 Potential.
FT DOMAIN 210 211 1.
FT REPEAT 210 211 1.
FT REPEAT 212 213 2.
FT REPEAT 214 215 3.
FT REPEAT 216 217 4.
FT REPEAT 218 219 5.
FT DOMAIN 268 312 OmpA-like.
FT DISULFID 322 336 By similarity.
SQ SEQUENCE 359 AA; 38426 MW; 13992A037C19758B CRC64;

Query Match 75.8%; Score 1381.5; DB 1; Length 359;
Best Local Similarity 78.4%; Pred No. 6e-98;
Matches 269; Conservative 24; Mismatches 43; Indels 7; Gaps 4;

QY 6 VLNAAPKNTWYAGKLGWSQVHDTGTFYNGFNQ--NNGPTRNDQLGAGAFGGYQVNPYL 63
DB 18 VAQAAPKNTWTGAKLGWSQVHDTGTFYNGYQNGIGNGPTHKDKLGAGAFGLYQANQYL 77

QY 64 GFEMCYDNLGRMAYKGSVDNGAFKAQGVLTAKLGYPIITDDLDIYTRLGGMWRADSKGN 123
DB 78 GFELGYDNLGRMPYKGSVNNNGAFKAQGVLTAKLGYPIITDDLDIYTRLGGMWRADSKAN 137

QY 124 YASTGVSRSEHDTGVSFVAGGVEAVTRDIATRLLEYQVNNIGDAGTVGTRPDNGMLSL 183
DB 138 YGRTQRLSDHDTGVSPIAAVGEVATLKNWATRLDYQFVSNIGDAGTVGTRPDNTMLSL 197

QY 184 GVSRYFGQED--AAPVAPAPAPAPAVATKHTLKSVDLNFNFKATLKPEGQQAALDQLYTQ 242
DB 198 GVSRYFGQDDVVAP--ADAPAPAPVETKRTFLKSDVLFNFNFKSTLKAEGQQAALDQLYTQ 255
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QY 243 LSNMPPKDGSAVVGLGYTRIGSBAYNOOLSEKRAQSVVDYLVAKGIPAGKISARGMGESN 302
DB 256 LSNMPPKDGSAVVGLGYTRIGSBAYNOOLSEKRAQSVVDYLVAKGIPAGKISARGMGESN 315
QY 303 PVTGNTCDNVKARA--ALIDCLAPDRRVEIEVKYKEVVTQPQ 343
DB 316 AVTGNTCGYSGRATKAQIVCLAPDRRVEIEVKYKEVVTQPQ 358

RESULT 15
Q6QT47 PRELIMINARY; PRT; 319 AA.
AC Q6QT47;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Outer membrane protein A (Fragment).
GN Name=ompA;
OS Salmonella gallinarum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=594;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB323;
RA Vega-Manriquez X., Martinez-Gomez D., Verdugo-Rodriguez A.;
RT "Avian serum proteins regulated expression of Salmonella gallinarum
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ompA family.
CC EMBL; AY526610; AAS18468.1; -.
CC GO; GO:0009288; C:flagellum (sensu Bacteria); IEA.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
CC GO; GO:0003774; F:motor activity; IEA.
CC GO; GO:0005198; F:structural molecule activity; IEA.
CC GO; GO:0001539; P:ciliary or flagellar motility; IEA.
CC InterPro; IPR006664; Bac_OmpA.
CC InterPro; IPR001035; MotY.
CC InterPro; IPR002368; OmpA.
CC InterPro; IPR006665; OmpA/MotB.
CC InterPro; IPR006690; OMPA LIKE.
CC InterPro; IPR000498; OmpA_tmem.
CC Pfam; PF00691; OmpA; 1.
CC Pfam; PF01389; OmpA membrane; 1.
CC PRINTS; PR01023; NAPLGMOTY.
CC PRINTS; PR01021; OMPADOMAIN.
CC PRINTS; PR01022; OUTRMMBRANEA.
CC ProDom; PD000930; OmpA/MotB; 1.
CC PROSITE; PS01068; OmpA; 1.
FT NON_TER 1 1
FT NON_TER 319 319
SQ SEQUENCE 319 AA; 34464 MW; 8A2B227DC4FF9CD CRC64;

Query Match 74.9%; Score 1364; DB 2; Length 319;
Best Local Similarity 81.1%; Pred No. 1.1e-96;
Matches 258; Conservative 26; Mismatches 26; Indels 8; Gaps 3;

QY 22 LGW--SOYHDTGTFYNGFNQNNNGPTRNDQLGAGAFGGYQVNPYLGFEMGYDNLGRMAYKG 79
DB 7 LTWRPPQVHDTGTFI-----HNDGPTDENQLGAGAFGGYQVNPYVFGFEMGYDNLGRMPYKG 61

QY 80 SVDNGAFKAQGVLTAKLGYPIITDDLDIYTRLGGMWRADSKGNVASTGYSRSEHDTGVS 139
DB 62 DNINGAYKAQGVLTAKLGYPIITDDLDVYTRLGGMWRADTKSNVPG-GPSTKDHDTGVS 120

QY 140 PVFAGGVEAVTRDIATRLLEYQVNNIGDAGTVGTRPDNGMLSLGVSRYFGQEDAAPVVA 199
DB 121 PVFAGGLEIATPPIATRLLEYQVNNIGDANTIGTRPDNGLLSVGVSRYFGQEDAAPVVA 180

QY 200 PAPAPAPAVATKHTLKSVDLNFNFKATLKPEGQQAALDQLYTQLSNMDPKDGSVAVLGYT 259
DB 200 PAPAPAPAVATKHTLKSVDLNFNFKATLKPEGQQAALDQLYTQLSNMDPKDGSVAVLGYT 259
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Db 181 PAPAPAPEVQTKHFTLKSDVLFNFKNSTLKPGEQALDQLYSQSLNLPDKGSGVVVLGFT 240
Qy 260 DRIGSEAYNQQLSEKRAQSVVDYLVAKGIPACKISARGMGESNPVTGNTCDNVKARAALI 319
Db 241 DRIGSDAYNQLSEKRAQSVVDYLKSGIPSDKISARGMGESNPVTGNTCDNVKFPRAALI 300
Qy 320 DCLAPDRRVEIEVKGYKE 337
Db 301 DCLAPDRRVEIEVKGVKD 318

RESULT 16
Q56CF0
ID Q66CF0 PRELIMINARY; PRT; 353 AA.
AC Q66CF0;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Putative outer membrane porin A protein precursor.
GN Name=ompA; Synonyms=con, tolG, tut; ORFNames=YPTB1453;
OS Yersinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=273123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 32953;
RX PubMed=15358858;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francoise V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RA "Insights into the genome evolution of Yersinia pestis through whole
RT genome comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; BX936398; CAH20693.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019867; C: outer membrane; IEA.
DR GO; GO:0015288; F: porin activity; IEA.
DR InterPro; IPR006664; Bac OmpA.
DR InterPro; IPR001035; MotY.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_tmam.
DR Pfam; PF00691; OmpA_1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01023; NAFEGMOTY.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBRANEA.
DR ProDom; PD000930; OmpA/MotB; 1.
KW Porin; Signal.
FT SIGNAL 1 22 Potential.
SQ SEQUENCE 353 AA; 37929 MW; 38D23EFD5466CBF CRC64;

Query Match 73.2%; Score 1334.5; DB 2; Length 353;
Best Local Similarity 75.4%; Pred. No. 2.4e-94;
Matches 257; Conservative 28; Mismatches 49; Indels 7; Gaps 4;

Qy 6 VLNAAPKDNWTYAGKLGWSQYHDTGTFYNGFNQNGPTRNDQLGAGAFGYQVNPYLGF 65
Db 18 VAQAAPKDNWTYTGKLGWSQYQDTG-----SIINNDGPTHKQDLGAGAFFGYQANQYLGF 73
Qy 66 EMGYDWMGRMAYKGSVDNGAFKAGQVLTAKLGYPIITDLDIYTRLGWVWRADSKGNYA 125
Db 74 EMGYDWMGRMPYKGDINNGAFKAGQVLAALKLSPVAQDLVDVYTRLGGLVWRADAKGSF- 132
Qy 126 STGVSR-SEHDTGSPVPFAGVGEVAVTRDIAIRLEYQWVNNIGDAGTVGTRPDNGMLSLG 184
Db 133 DGGLDRASGHDTVGSPVLVAGAEYATWTKWATREYQWVNNIGRETGVARPDNGLLSVG 192
Qy 185 VSYRFGQED-AAPVAPAPAPAPAEVATKHFTLKSDVLFNFKNATLKPEGOALDQLYTOL 243
Qy 193 VSYRFGQEDAAPIVAPTAPAPITVDTKRFTLKSDVLFNFKNATLKPEGOALDQLYAOL 252

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Db 193 VSYRFGQEDAAPIVAPTAPAPITVDTKRFTLKSDVLFNFKNATLKPEGOALDQLYAOL 252
Qy 244 SNMPPKDGSAVVLGVTRDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPACKISARGMGESNP 303
Db 253 SSIDPKDGSVVVLGFADRIQGPAPNALSQRRASVVDYLVKGI PADKITARGEGQANP 312
Qy 304 VTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPOA 344
Db 313 VTGNTCDNVKARAALIECLAPDRRVEIEVKGYKEVVTQPOA 353

RESULT 17
Q8ZG77
ID Q8ZG77 PRELIMINARY; PRT; 353 AA.
AC Q8ZG77;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE Putative outer membrane porin A protein.
GN Name=ompA; Synonyms=con, tolG, tut; OrderedLocusNames=YPO1435;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Tittball R.W., Hoiden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagsels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; AJ414148; CAC90263.1; -.
DR PIR; AD0175; AD0175.
DR HSP; P02934; 1QJP.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0015288; F: porin activity; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR Pfam; PF00691; OmpA_1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBRANEA.
DR ProDom; PD000930; OmpA/MotB; 1.
KW Complete proteome; Porin.
SQ SEQUENCE 353 AA; 37929 MW; 38D23EFD5466CBF CRC64;

Query Match 73.2%; Score 1334.5; DB 2; Length 353;
Best Local Similarity 75.4%; Pred. No. 2.4e-94;
Matches 257; Conservative 28; Mismatches 49; Indels 7; Gaps 4;

Qy 6 VLNAAPKDNWTYAGKLGWSQYHDTGTFYNGFNQNGPTRNDQLGAGAFGYQVNPYLGF 65
Db 18 VAQAAPKDNWTYTGKLGWSQYQDTG-----SIINNDGPTHKQDLGAGAFFGYQANQYLGF 73
Qy 66 EMGYDWMGRMAYKGSVDNGAFKAGQVLTAKLGYPIITDLDIYTRLGWVWRADSKGNYA 125
Db 74 EMGYDWMGRMPYKGDINNGAFKAGQVLAALKLSPVAQDLVDVYTRLGGLVWRADAKGSF- 132
Qy 126 STGVSR-SEHDTGSPVPFAGVGEVAVTRDIAIRLEYQWVNNIGDAGTVGTRPDNGMLSLG 184
Db 133 DGGLDRASGHDTVGSPVLVAGAEYATWTKWATREYQWVNNIGRETGVARPDNGLLSVG 192
Qy 185 VSYRFGQED-AAPVAPAPAPAPAEVATKHFTLKSDVLFNFKNATLKPEGOALDQLYTOL 243
Qy 193 VSYRFGQEDAAPIVAPTAPAPITVDTKRFTLKSDVLFNFKNATLKPEGOALDQLYAOL 252

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QY 244 SNMPPKDSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPACKISARGMGESNP 303
DB 253 SSIDPKDGSVVVLGFADRIQGPAPNALSORRADSVRDYLVSKGIPADKITARGEGQANP 312
QY 304 VTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVWTPQQA 344
DB 313 VTGNTCDNVKARAALIECLAPDRRVEIEVKGYKEVWTPQQA 353

RESULT 18
Q8D056 PRELIMINARY; PRT; 363 AA.
AC Q8D056; Q74V12;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Outer membrane porin A.
GN Name=ompA; Synonyms=ompA1; OrderedLocusNames=YP1326, Y2735;
OS Yersinia pestis
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1128/JB.194.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=91001 / Biovar Mediaevalis;
RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
RA Yang R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; AE013876; AAM86287.1; -.
DR EMBL; AE017132; AAS61569.1; -.
DR HSSP; P02934; 1QJP.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBRANEA.
DR ProDom; PD000930; OmpA/MotB; 1.
KW Porin.
SQ SEQUENCE 363 AA; 39273 MW; DCBB6CF480E61A24 CRC64;

Query Match 73.2%; Score 1334.5; DB 2; Length 363;
Best Local Similarity 75.4%; Pred. No. 2.5e-94;
Matches 257; Conservative 28; Mismatches 49; Indels 7; Gaps 4;

QY 6 VLNAAPKNTWYAGCKLGSQYHDTGFGYNGFQNNQTRNDOLGAGAFGCVQNPYLGF 65
DB 28 VAQAAPKNTWYTGKGLGSQYQDTG-----STIINDGPTHKDLGAGAFFGYQANQYLGF 83
QY 66 EMGYDNLGRMPYKGDINNGAFKAQGVQLAALKSYPAQDLDDVYTRLGGLVVRADAKGSF - 142
DB 126 STGVSR-SEHDTGVSVPFAGGVFWAVTRD:ATRLLEYQWVNNIGDAGTVGTRPDNGMLSLG 184
DB 143 DGGLDRAAGSHDGTGVSPLVALGAEYAWTKNATWATRMEXQYVNNIGDRETVGARPDNGLLSVG 202
QY 185 VSYRFGQED--AAPVWAPAPAPAEVATKHTFLKSDVLFNFENKATLKEPQGQALDQLYTOL 243
DB 203 VSYRFGQEDAAAPIVATPAPAPIVDTRFKRFLKSDVLFNFENKATLKEPQGQALDQLYTOL 262
QY 244 SNMPPKDSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPACKISARGMGESNP 303
DB 263 SSIDPKDGSVVVLGFADRIQGPAPNALSORRADSVRDYLVSKGIPADKITARGEGQANP 322
QY 304 VTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVWTPQQA 344
DB 323 VTGNTCDNVKARAALIECLAPDRRVEIEVKGYKEVWTPQQA 363

RESULT 19
Q6D6D4 PRELIMINARY; PRT; 366 AA.
AC Q6D6D4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Outer-membrane protein A.
GN Name=ompA; OrderedLocusNames=ECA1751;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Scri 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Heleva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jang S., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; BX950851; CAG74656.1; -.
DR GO; GO:0009288; C:flagellum (sensu Bacteria); IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0001539; P:ciliary or flagellar motility; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR001035; MotY.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR006690; OMPA_LIKE.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01023; NAFLNGMOTY.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBRANEA.
DR ProDom; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OMPA; 1.
KW Complete proteome.
SQ SEQUENCE 366 AA; 39013 MW; 7BD65E03C6179F25 CRC64;

Query Match 72.2%; Score 1315; DB 2; Length 366;
Best Local Similarity 72.2%; Pred. No. 8e-93;
Matches 255; Conservative 40; Mismatches 40; Indels 18; Gaps 7;

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Qy	6	V L N A P K O N T W Y A G K L G W S O H D T G F Y V G N G F O N - N N G P T R N D Q L G A G A P G V G Y V N N P Y L G 64
Db	18	V A O A A P K O N T W Y T G G K L G Y S O P H D T G F Y G N G Y T D V N N N P I K S - K L G A F A P V G Y Q A N P Y L G 76
Qy	65	F E M G Y D W L G R M A Y K G S - - - - V D N G A F K A Q G V O L T A K L G Y P I T D D L D I Y T R L G M W R - - - 117
Db	77	F E M G Y D W L G R M K Y A G S T A N P A D S A S L K A Q G I Q L A A K L S Y P V L P D L D V Y T R L G M W R V D T 136
Qy	118	- A D S K G N Y A S T G V S R S E H D T G V S P V F A G G V E M A Y T R D I A T R L E Y O W N N I G D A G T V G T R P 176
Db	137	H A D R S N H L - - - - - N N D D T G V S P L A A I G I B Y A I D K M W A T R V D Y Q W V S N I G D A G T V G A R P 190
Qy	177	D N G M L S L G V S Y R F G O E D - A A P W A P A - P A P A P E V A T K F T L K S D V L F N F N K A T L K P E Q 233
Db	191	D N W L M S V G L S Y R F G Q D R V A P V V A P A P T P A P A P V E T K R F T L K S D V L F N F N K A T L K A E Q 250
Qy	234	Q A L D Q L Y T Q L S N M D P K G S A V V L G Y T D R I G S E A Y N Q O L S E K R A Q S V V D Y L V A K G I P A G K I 293
Db	251	Q S I L D Q L Y T Q L S S L D P K G S V V V L G F S D R L G S E Q Y N Q A L S E K R A Q S V V D Y L V S K G I P A N K V 310
Qy	294	S A R G M G E S N P V T G N T C D N V - - - - - K A R A A L I D C L A P D R R V E I V E K G Y K E V V T Q P O A 344
Db	311	S A R G L K G S O P V T G S T C D N V Y K O G R A A T K A O L I D C L A P D R R V E I V E I G I K O V T Q P O A 367

RESULT 22

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Q99114      PRELIMINARY;      PRT;      238 AA.
ID   Q99114
AC   Q99114;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Outer membrane protein II (Fragment).
DE   Name=ompA;
OS   Escherichia vulneris.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
NCBI_TaxID=566;
[1]
SEQUENCE FROM N.A.
RP   MEDLINE=92065252; PubMed=1955870;
RX   Lawrence J.G., Ochman H., Hartl D.L.;
RT   "Molecular and evolutionary relationships among enteric bacteria.";
RL   J. Gen. Microbiol. 137:1911-1921(1991).
CC   -1- SIMILARITY: Belongs to the ompA family.
EMBL: MG3348; AAA24233.1; -.
PIR: I62385; I62385.
HSSP: P02934; IQJP.
GO: GO:0016021; C: integral to membrane; IEA.
GO: GO:0009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.
GO: GO:0005198; F: structural molecule activity; IEA.
InterPro: IPR006664; Bac OmpA.
InterPro: IPR002368; OmpA.
InterPro: IPR006665; OmpA/MotB.
InterPro: IPR006690; OmpA LIKE.
InterPro: IPR000498; OmpA_tmem.
Pfam: PF00691; OmpA; 1.
Pfam: PF01389; OmpA membrane; 1.
PRINTS: PR01021; OMPADOMAIN.
PRINTS: PR01022; OUTRMBRANEA.
ProDom: PD000930; OmpA/MotB; 1.
PROSITE: PS01068; OmpA; 1.
FT   NON_TER      1
FT   NON_TER      238
SQ   SEQUENCE      238 AA; 25604 MW; B05D116C01DD9733 CRC64;

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Qy	153	DIATRL	QVWNNIGDAGTGTGTRPDNGMLSLGVS	YRFGQEDAAAPV	VAPAPAPAEVATKH	212				
Db	56	DIATRL	QVWNNIGDAGTGTGTRPDNGMLSGVS	YRFGQENAPV	VAPAPAPAEVTTKT	115				
Qy	213	FTLKSD	VLNFNKATLKPEGOQALDQLYTQLSNM	PKDGS	AVVLGYTDRIGSEAYNQOLS	272				
Db	116	FTLKSD	VLNFNKATLKPEGOQALDQLYTQLSNM	PKDGS	AVVLGYTDRIGSBOYNOKLS	175				
Qy	273	EKRAQS	VVDVYLVAKGIPAGKISARGMESNPVTGNT	CDNKKARAALIDCLAP	RRVVEIEV	332				
Db	176	EKRAQS	VVDVYLVAKGIPANKISARGMESDPVTGNT	CDNKKARAALIDCLAP	RRVRAIEV	235				
Qy	333	KGy	335							
Db	236	KGy	238							
RESULT 23										
ID	Q47880	PRELIMINARY;		PRT;	244	AA.				
AC	Q47880;									
DT	01-NOV-1996	(TrEMBLrel. 01, Created)								
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)								
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)								
DE	Outer membrane protein II (Fragment).									
GN	Name=ompA;									
OS	Escherichia vulneris.									
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;									
OC	Enterobacteriaceae; Escherichia.									
OX	NCBI_TaxID=566;									
RP	[1]									
RN	SEQUENCE FROM N.A.									
RX	MEDLINE=92065252; PubMed=1955870;									
RA	Lawrence J.G., Ochman H., Hartl D.L.;									
RT	"Molecular and evolutionary relationships among enteric bacteria.";									
RL	J. Gen. Microbiol. 137:1911-1921(1991).									
CC	-1- SIMILARITY: Belongs to the ompA family.									
DR	EMBL; M63350; AAA24241.1; -.									
DR	PIN; I62393; I62393.									
DR	HSP; P02934; I0JP.									
DR	GO; GO:0016021; C:integral to membrane; IEA.									
DR	GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.									
DR	GO; GO:0005198; F:structural molecule activity; IEA.									
DR	InterPro; IPR006664; Bac_OmpA.									
DR	InterPro; IPR002368; OmpA.									
DR	InterPro; IPR006665; OmpA/MotB.									
DR	InterPro; IPR006690; OMPA LIKE.									
DR	InterPro; IPR000498; OmpA_tmem.									
DR	Pfam; PF00691; OmpA; 1.									
DR	Pfam; PF01389; OmpA_membrane; 1.									
DR	PRINTS; PR01021; OMPADOMAIN.									
DR	PRINTS; PR01022; OUTRMMBRANA.									
DR	ProDom; PD000930; OmpA/MotB; 1.									
DR	PROSITE; PS01068; OMPA; 1.									
FT	NON_TER	1	244							
FT	NON_TER	244	244							
SQ	SEQUENCE	244	AA; 26275	MW; C6D068A6A0916179	CRC64;					
Query Match										
Best Local Similarity		61.1%;	Score 1112.5;	DB 2; Length 244;						
Matches 212;		Conservative	15;	Mismatches 15;	Indels 1;	Gaps 1;				
Qy	93	LTAKLG	YPIITDLDLDIYTRLG	GMWWRADSKGN	YASTGVSRSEHDTGVS	PVAGGVWAVTR 152				
Db	1	LTAKLG	YPIITDLDLDIYTRLG	GMWWRADSKAQV	POTGTGASFKDHD	TGVSFPVAGGVWAVTR 60				
Qy	153	DIATRL	QVWNNIGDAGTGTGTRPDNGMLSLGVS	YRFGQEDAAAPV	VAPAPAPAEV					

Db 121 HFTLKSDFVFNFKATLKPGEQALDQMYSQLSNDPKDGSVVVLGFTDRIGSDAYNOGL 180

Qy 272 SEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNKARALIDCLAPDRRVEIE 331

Db 181 SEKRAQSVVDYLISGIPSNKISARGMGESNPVTGNTCDNKARPALIDCLAPDRRVEIE 240

Qy 332 VKG 334

Db 241 VKG 243

RESULT 24

OMP_A_ESCFE

ID OMP_A_ESCFE STANDARD; PRT; 243 AA.

AC P24747;

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Outer membrane protein A (Outer membrane protein II) (Fragment).

GN Name=ompA;

OS Escherichia fergusonii.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=564;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 35469, ATCC 35471, and ATCC 35472;

RX MEDLINE=92065252; PubMed=1955870;

RA Lawrence J.G., Ochman H., Hartl D.L.;

RT "Molecular and evolutionary relationships among enteric bacteria.";

RL J. Gen. Microbiol. 137:1911-1921(1991).

CC -!- FUNCTION: Required for the action of colicins K and L and for the

CC stabilization of mating aggregates in conjugation. Serves as a

CC receptor for a number of T-even like phages. Also acts as a porin

CC with low permeability that allows slow penetration of small

CC solutes (by similarity).

CC -!- SUBUNIT: Monomer (Probable).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.

CC -!- MISCELLANEOUS: The sequence shown is that of strains ATCC 35471

CC and ATCC 35472.

CC -!- SIMILARITY: Belongs to the ompA family.

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CC or send an email to license@isb-sib.ch).

CC EMBL; M63352; AAA24236.1; -.

DR EMBL; M63351; AAA24232.1; -.

DR EMBL; M63353; AAA24240.1; -.

DR PIR; I62388; I62388.

DR PIR; I84531; I84531.

DR HSSP; P02934; IQJP.

DR InterPro; IPR006664; Bac OmpA.

DR InterPro; IPR002368; OmpA.

DR InterPro; IPR006665; OmpA/MotB.

DR InterPro; IPR006690; OmpA LIKE.

DR Pfam; PF00691; OmpA; 1.

DR Pfam; PF01389; OmpA membrane; 1.

DR PRINTS; PR01021; OMPADOMAIN.

DR PRODOM; PD000930; OmpA/MotB; 1.

DR PROSITE; PS01068; OMPA; 1.

KW Conjugation; Outer membrane; Phage recognition; Porin; Repeat;

KW Transmembrane.

FT NON TER 1 8 Potential.

FT TRANSMEM <1 8 Potential.

FT TRANSMEM 12 27 Potential.

FT TRANSMEM 48 59 Potential.

FT TRANSMEM 65 81 Potential.

FT TRANSMEM 87 98 Potential.

FT DOMAIN 107 114

FT REPEAT 107 108

FT REPEAT 109 110

FT REPEAT 111 112

FT REPEAT 113 114

FT DOMAIN 163 207

FT DISULFID 217 229

FT VARIANT 39 39

FT NON TER 243 243

SQ SEQUENCE 243 AA; 26144 MW; B89F7FC29D42E3AB CRC64;

Query Match 61.0%; Score 1111; DB 1; Length 243;

Best Local Similarity 87.2%; Pred. No. 2.3e-77;

Matches 211; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

Qy 93 LTAKLGYPIITDDLDIYTRLGGMVWRADSKGNVASTGVSRSRSHDTGVSVPFAGGVEMAVTR 152

Db 1 LTAKLGYPIITDDLDIYTRLGGMVWRADTKAHNNVTGSEKKNHDTGVSVPFAGGVEMAVTR 60

Qy 153 DIATRLQYQVNNIGDAGTVGTRPDNGMLSIGVSYRFGQEDAAAPVAPAPAPAPAPAPATKH 212

Db 61 EIATRLQYQVNNIGDANTIGTRPDNGLLSLGVSYRFGQGEAAPVAPAPAPAPAPAPATKH 120

Qy 213 FTLKSDVLFNFKATLKPGEQALDQLYTQLSNMDPKDGSAAVLGYTDRIGSEAYNQOLS 272

Db 121 FTLKSDVLFNFKATLKPGEQALDQLYSQLSNDPKDGSVVVLGFTDRIGSDAYNOGLS 180

Qy 273 EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNKARALIDCLAPDRRVEIEV 332

Db 181 EKRAQSVVDYLISGIPSNKISARGMGESNPVTGNTCDNKARALIDCLAPDRRVEIEV 240

Qy 333 KG 334

Db 241 KG 242

RESULT 25

Q99115

ID Q99115 PRELIMINARY; PRT; 244 AA.

AC Q99115;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Outer membrane protein II (Fragment).

GN Name=ompA;

OS Escherichia vulneris.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=566;

RN [1]

RX SEQUENCE FROM N.A.

RP MEDLINE=92065252; PubMed=1955870;

RA Lawrence J.G., Ochman H., Hartl D.L.;

RT "Molecular and evolutionary relationships among enteric bacteria.";

RL J. Gen. Microbiol. 137:1911-1921(1991).

CC -!- SIMILARITY: Belongs to the ompA family.

DR EMBL; M63349; AAA24237.1; -.

DR PIR; I62389; I62389.

DR HSSP; P02934; IQJP.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR006664; Bac OmpA.

DR InterPro; IPR002368; OmpA.

DR InterPro; IPR006665; OmpA/MotB.

DR InterPro; IPR006690; OmpA LIKE.

DR InterPro; IPR000498; OmpA_tmem.

DR Pfam; PF00691; OmpA; 1.

DR Pfam; PF01389; OmpA membrane; 1.

DR PRINTS; PR01021; OMPADOMAIN.

DR PRODOM; PD000930; OmpA/MotB; 1.

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DR PROSITE; PS01068; OMPA; 1.
FT NON_TER 1
FT NON_TER 244
SQ SEQUENCE 244 AA; 26237 MW; C4D18BB27656EDBA CRC64;

Query Match 60.9%; Score 1110.5; DB 2; Length 244;
Best Local Similarity 86.8%; Pred. No. 2.5e-77;
Matches 211; Conservative 16; Mismatches 15; Indels 1; Gaps 1;

QY 93 LTAKLGYPIITDLDIYTRLGGMWRADSKGNVASTGVSRSEHDTGVSVPFAGGVEMAVTR 152
DB 1 LTAKLGYPIITDLDIYTRLGGMWRADSKGVGGTGSFKDHDITGVSVPFAGGVEMAVTR 60

QY 153 DIATRLVQWNNIGDAGTGTTRPDNGMLSGVSYREG-QEDAAPVAPAPAPAPEVATK 211
DB 61 DIATRLVQWNNIGDAGTGTTRPDNGMLSGVSYREGQEDVAPVAPAPAPAPQVSTK 120

QY 212 HFTLKSDVLFNFKATLKPEGQALDQYLTQLSNMDPKDGSAVVLGYTDRIGSBAYNQOL 271
DB 121 HFTLKSDVLFNFKATLKPEGQALDQYLSQLSNLDPKDGSAVVLGYTDRIGSBAYNQOL 180

QY 272 SEKRAQSVVDVLYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIE 331
DB 181 SEKRAQSVVDVLYLISKIPSNKISARGMGESNPVTGNTCDNVKARPALIDCLAPDRRVEIE 240

QY 332 VKG 334
DB 241 VKG 243

RESULT 26
OMPA_ESCHE STANDARD; PRT; 243 AA.
AC F24754;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Outer membrane protein A (Outer membrane protein II) (Fragment).
GN Name=ompA;
OS Escherichia hermannii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33650, and ATCC 33652;
RX MEDLINE=92065252; PubMed=1955870;
RA Lawrence J.G., Ochman H., Hartl D.L.;
RT "Molecular and evolutionary relationships among enteric bacteria.";
RL J. Gen. Microbiol. 137:1911-1921(1991).
CC -!- FUNCTION: Required for the action of colicins K and L and for the
CC stabilization of mating aggregates in conjugation. Serves as a
CC receptor for a number of T-even like phages. Also acts as a porin
CC with low permeability that allows slow penetration of small
CC solutes (By similarity).
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -!- SIMILARITY: Belongs to the ompA family.
CC -----
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CC -----
DB EMBL; M63346; AAA24234.1; -.
DR EMBL; M63347; AAA24238.1; -.
DR PIR; I62386; 162386.
DR HSSP; P02934; 1BXW.
DR InterPro; IPR006664; Bac OmpA.
DR InterPro; IPR002368; OmpA.

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DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR006690; OMPA LIKE.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR ProDom; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OMPA; 1.
KW Conjugation; Outer membrane; Phage recognition; Porin; Repeat;
KW Transmembrane.
FT NON_TER 1
FT TRANSMEM <1 8 Potential.
FT TRANSMEM 12 27 Potential.
FT TRANSMEM 47 58 Potential.
FT TRANSMEM 64 80 Potential.
FT TRANSMEM 86 97 Potential.
FT DOMAIN 107 114 1.
FT REPEAT 107 108 1.
FT REPEAT 109 110 2.
FT REPEAT 111 112 3.
FT REPEAT 113 114 4.
FT DOMAIN 163 207 OmpA-like.
FT DISULFID 217 229 By similarity.
FT NON_TER 243 243
SQ SEQUENCE 243 AA; 26202 MW; AA6CB6BA390D1E9D CRC64;

Query Match 60.7%; Score 1106; DB 1; Length 243;
Best Local Similarity 87.7%; Pred. No. 5.5e-77;
Matches 213; Conservative 14; Mismatches 14; Indels 2; Gaps 2;

QY 93 LTAKLGYPIITDLDIYTRLGGMWRADSKGNVASTGVSRSEHDTGVSVPFAGGVEMAVTR 152
DB 1 LTAKLGYPIITDLDIYTRLGGMWRADSKYNIPG-GASFKDHDITGVSVPFAGGVEMAVTR 59

QY 153 DIATRLVQWNNIGDAGTGTTRPDNGMLSGVSYREGQED-AAPVAPAPAPAPEVATK 211
DB 60 DIATRLVQWNNIGDANTVGTTRPDNGLLSGVSYREGQEEAAPVAPAPAPEVQTK 119

QY 212 HFTLKSDVLFNFKATLKPEGQALDQYLTQLSNMDPKDGSAVVLGYTDRIGSBAYNQOL 271
DB 120 HFTLKSDVLFNFKATLKPEGQALDQYLTQLSNLDPRDGSVVVLGYTDRIGSBAYNQOL 179

QY 272 SEKRAQSVVDVLYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIE 331
DB 180 SEKRAQSVVDVLYLISKIPSDKISARGMGESNPVTGNTCDNVKPRALIDCLAPDRRVEIE 239

QY 332 VKG 334
DB 240 VKG 242

RESULT 27
Q99123
ID Q99123 PRELIMINARY; PRT; 238 AA.
AC Q99123;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein II (Fragment).
GN Name=ompA;
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=548;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E482;
RX MEDLINE=92065252; PubMed=1955870;
RA Lawrence J.G., Ochman H., Hartl D.L.;
RT "Molecular and evolutionary relationships among enteric bacteria.";
RL J. Gen. Microbiol. 137:1911-1921(1991).
CC -!- SIMILARITY: Belongs to the ompA family.
CC EMBL; M63356; AAA24807.1; -.

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DR HSP; P02934; 1QJP.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_LIKE.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR ProDom; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OmpA; 1.
FT NON_TER 1
FT NON_TER 238
SQ SEQUENCE 238 AA; 25554 MW; BCDP6AP25240202B CRC64;

Query Match 60.1%; Score 1095.5; DB 2; Length 238;
Best Local Similarity 86.0%; Pred. No. 3.5e-76;
Matches 208; Conservative 15; Mismatches 14; Indels 5; Gaps 1;

Qy 93 LTKALGYPIITDDLDIYTRLGGMVWRADSKGNVASTGVSRSSEHDTGVSVPFAGGVEWAVTR 152
Db 1 LTKALGYPIITDDLDIYTRLGGMVWRADT-----SNSIAGDDHDTGVSVPFAGGVEWAVTR 55

Qy 153 DIATRLYQWNNIGDAGTGTGTRPDNGMLSLGVSRFGQEDAAPVVPAPAPAPAEVATKH 212
Db 56 DIATRLYQWNNIGDAGTGTGTRPDNGMLSLGVSRFGQEDAAPVVPAPAPAEVATKH 115

Qy 213 FTLKSDVLFNFNFKATLKPEGGQALDQLYTQLSNMDPKDGSVAVLGYTDRIGSEAYNQOLS 272
Db 116 FTLKSDVLFNFNFKATLKPEGGQALDQLYTQLSNMDPKDGSVAVLGYTDRIGSDAYNQOLS 175

Qy 273 EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKRAALDCLAPDRRVEIEV 332
Db 176 EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKRAALDCLAPDRRVEIEV 235

Qy 333 KG 334
Db 236 KG 237

RESULT 28
OMPA_ESCBL STANDARD; PRT; 241 AA.
AC Q99124; Q03617;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Outer membrane protein A (Outer membrane protein II) (Fragment).
GN Name=ompA;
OS Escherichia blattae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=563;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29907, ATCC 33429, and ATCC 33430;
RX MEDLINE=92065252; PubMed=1955870;
RA Lawrence J.G., Ochman H., Hartl D.L.;
RT "Molecular and evolutionary relationships among enteric bacteria.";
RL J. Gen. Microbiol. 137:1911-1921(1991).
CC -!- FUNCTION: Required for the action of colicins K and L and for the
CC stabilization of mating aggregates in conjugation. Serves as a
CC receptor for a number of T-even like phages. Also acts as a porin
CC with low permeability that allows slow penetration of small
CC solutes (by similarity).
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -!- MISCELLANEOUS: The sequence shown is that of strain ATCC 33429.
CC -!- SIMILARITY: Belongs to the ompA family.

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CC -----
DR EMBL; M63343; AAA24235.1; -.
DR EMBL; M63344; AAA24239.1; -.
DR EMBL; M63345; AAA24242.1; -.
DR PIR; I62387; I62387.
DR PIR; I62391; I62391.
DR PIR; I62394; I62394.
DR HSP; P02934; 1QJP.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR006690; OMPA_LIKE.
DR InterPro; IPR000498; OmpA_tmam.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR ProDom; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OmpA; 1.
KW Conjugation; Outer membrane; Phage recognition; Porin; Repeat;
KW Transmembrane.
FT NON_TER 1
FT TRANSMEM <1 8 Potential.
FT TRANSMEM 12 27 Potential.
FT TRANSMEM 46 57 Potential.
FT TRANSMEM 63 79 Potential.
FT TRANSMEM 85 96 Potential.
FT DOMAIN 105 112 4 X 2 AA tandem repeats of A-P.
FT REPEAT 105 106 1.
FT REPEAT 107 108 2.
FT REPEAT 109 110 3.
FT REPEAT 111 112 4.
FT DOMAIN 161 205 OmpA-like.
FT DISULFID 215 227 By similarity.
FT VARIANT 33 33 V -> G (in strain ATCC 29907).
FT VARIANT 56 56 W -> M (in strain ATCC 33430).
FT VARIANT 101 101 Missing (in strain ATCC 33430).
FT VARIANT 213 213 N -> S (in strain ATCC 29907 and strain
FT ATCC 33430).
FT VARIANT 220 220 K -> Q (in strain ATCC 29907 and strain
FT ATCC 33430).
FT NON_TER 241
SQ SEQUENCE 241 AA; 25986 MW; 7C81CC0CCD5F1C40 CRC64;

Query Match 59.8%; Score 1089; DB 1; Length 241;
Best Local Similarity 86.0%; Pred. No. 1.1e-75;
Matches 208; Conservative 17; Mismatches 15; Indels 2; Gaps 1;

Qy 93 LTKALGYPIITDDLDIYTRLGGMVWRADSKGNVASTGVSRSSEHDTGVSVPFAGGVEWAVTR 152
Db 1 LTKALGYPIITDDLDIYTRLGGMVWRADAKNNV--VGGDRSNHDTGVSVPFAGGVEWAVTP 58

Qy 153 DIATRLYQWNNIGDAGTGTGTRPDNGMLSLGVSRFGQEDAAPVVPAPAPAEVATKH 212
Db 59 SIATRLYQWNNIGDAGTGTGTRPDNGMLSLGVSRFGQEDAAPVVPAPAPAEVATKH 118

Qy 213 FTLKSDVLFNFNFKATLKPEGGQALDQLYTQLSNMDPKDGSVAVLGYTDRIGSEAYNQOLS 272
Db 119 FTLKSDVLFNFNFKATLKPEGGQALDQLYTQLSNMDPKDGSVAVLGYTDRIGSDAYNQOLS 178

Qy 273 EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKRAALDCLAPDRRVEIEV 332
Db 179 QKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKRAALDCLAPDRRVEIEV 238

Qy 333 KG 334

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Db      239 KG 240

RESULT 29
OMPA_CITFR STANDARD; PRT; 238 AA.
AC P24016;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Outer membrane protein A (Outer membrane protein II) (Fragment).
GN Name=OmpA;
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OS60;
RX MEDLINE=92065252; PubMed=1955870;
RA Lawrence J.G., Ochman H., Hartl D.L.;
RT "Molecular and evolutionary relationships among enteric bacteria.";
RL J. Gen. Microbiol. 137:1911-1921(1991).
CC -!- FUNCTION: Required for the action of colicins K and L and for the
CC stabilization of mating aggregates in conjugation. Serves as a
CC receptor for a number of T-even like phages. Also acts as a porin
CC with low permeability that allows slow penetration of small
CC solutes (By similarity).
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -!- SIMILARITY: Belongs to the OmpA family.
CC -----
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CC -----
DR EMBL; M63354; AAA23095.1; -.
DR PIR; I40703; I40703.
DR HSSP; P02934; 1QJP.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR006690; OmpA LIKE.
DR InterPro; IPR000498; OmpA_tmern.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR ProDom; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OMPA; 1.
KW Configuration; Outer membrane; Phage recognition; Porin; Repeat;
KW Transmembrane.
FT NON_TER 1
FT TRANSMEM <1
FT TRANSMEM 12
FT TRANSMEM 27
FT TRANSMEM 43
FT TRANSMEM 54
FT TRANSMEM 60
FT TRANSMEM 76
FT TRANSMEM 82
FT TRANSMEM 93
FT DOMAIN 104
FT DOMAIN 109
FT REPEAT 104
FT REPEAT 105
FT REPEAT 106
FT REPEAT 107
FT REPEAT 108
FT REPEAT 109
FT REPEAT 158
FT REPEAT 159
FT REPEAT 158
FT DISULFID 212
FT NON_TER 238
FT SEQUENCE 238 AA; 25664 MW; 66EA136D73A3F286 CRC64;

Query Match 58.0%; Score 1056.5; DB 1; Length 238;
Best Local Similarity 84.8%; Pred. No. 3.4e-73;
Matches 206; Conservative 16; Mismatches 14; Indels 7; Gaps 3;

Db      239 KG 240

RESULT 30
Q9L6I9 PRELIMINARY; PRT; 249 AA.
AC Q9L6I9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Outer membrane protein A (Fragment).
GN Name=OmpA;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=QC;
RA Wang Y., Kim K.S.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF234270; AAF37888.1; -.
DR HSSP; P02934; 1QJP.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_tmern.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01022; OUTRMBRANE.
DR ProDom; PD000930; OmpA/MotB; 1.
FT NON_TER 249
FT SEQUENCE 249 AA; 26790 MW; 94D2CC00DDB9D1D0 CRC64;

Query Match 57.2%; Score 1042; DB 2; Length 249;
Best Local Similarity 80.7%; Pred. No. 4.8e-72;
Matches 192; Conservative 19; Mismatches 21; Indels 6; Gaps 2;

Qy      6 VLNAAPKDNWTYAGGKLGWSQYHDTGFYGNNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
Db      18 VAQAAPKDNWTYAGKLGWSQYHDTGFI-----HNDGPTHEHQAGAGFGGYQVNPYGVF 72

Qy      66 EMGYDWLGRMAYKSGVDNGAFKAGVOLTKAGLYPIITDDLDIYTRLGGMWRADSKGNYA 125
Db      73 EMGYDWLGRMEYKGDNINGAYKAGVOLTKAGLYPIITDDLDIYTRLGGMWRADSKGNYV 132

Qy      126 STGYSRSEHDTGVSPFAGGVEMAVTRDIAIRLQYQVNNIGDAGTVGTRPDNGMLSLGV 185
Db      133 G-GFSTKDHDTGVSPFAGGVEMAVTRDIAIRLQYQVNNIGDAGTVGTRPDNGMLSLGV 191

Qy      186 SYRFGQEDAAFPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 243

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[illegible]

RESULT 36	
Q6WAF9	PRELIMINARY; PRT; 162 AA.
ID	
AC	Q6WAF9;
DT	05-JUL-2004 (TRENBLrel. 27, Created)
DT	05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE	Outer membrane protein II (Fragment).
DE	Name=ompA;
GN	Klebsiella pneumoniae.
OS	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Klebsiella.
OC	NCBI_TaxID=573;
OX	[1]
RN	SEQUENCE FROM N.A.
RP	
RC	STRAIN=MISC208;
RX	MEDLINE=23001863; PubMed=14640415;
RA	Wertz J.E., Goldstone C., Gordon D.M., Riley M.A.;
RT	"A molecular phylogeny of enteric bacteria and implications for a
RT	bacterial species concept ";
RL	J. Evol. Biol. 16:1236-1248(2003).
CC	-1- SIMILARITY: Belongs to the ompA family.
CC	EMBL; AY301194; AAQ96088.1; -.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR	GO; GO:0005198; F:structural molecule activity; IEA.
DR	InterPro; IPR006664; Bac_OmpA.
DR	InterPro; IPR002368; OmpA.
DR	InterPro; IPR006665; OmpA/MotB.
DR	InterPro; IPR000498; OmpA_tmem.
DR	Pfam; PF00691; OmpA; 1.
DR	Pfam; PF01389; OmpA membrane; 1.
DR	PRINTS; PR01021; OMPADOMAIN.
DR	PRINTS; PR01022; OUTRMMBRANA.
DR	ProDom; PD000930; OmpA/MotB; 1.
FT	NON_TER 1
FT	NON_TER 162
SO	SEQUENCE 162 AA; 17383 MW; 9598BE6CA6BF13F7 CRC64;

Query Match	46.3%	Score 843;	DB 2;	Length 162;
Best Local Similarity	98.8%	Pred. NO. 5.5e-57;		
Matches 160;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	103	DDLDIYRLGGVWVRADSKGNVYASGVSRSHDTCVSPVAGGVGEVWATRIATKLEYQW	162	
Db	1	DDLDIYRLGGVWVRADSKGNVYASGVSRSHDTCVSPVAGGVGEVWATRIATKLEYQW	60	
Qy	163	VNNITGDAGTGVCTRPDNGMLSLGVSYRFQGEADAAPVWAPAPAPAEVATKFTFLKSDVLFN	222	

D6	61	VNNIGDAGTGTTRPDNCKMLSGVSYRFGQEDAAAPVAPAPAPAEVATKHFTLKSVDVLFN	120
QY	223	FNKATLPPEGQQALDQLYTQLSNMDPKDGSAVILGYTDRIGS	264
		:	
D6	121	FNKATLAPEGQALDQLYTQLSNMDPKDGSAVVVGFTDRIGS	162
RESULT 37			
ID	Q6WAGO	PRELIMINARY;	PRT; 162 AA.
AC	Q6WAGO;		
DT	05-JUL-2004	(TrEMBLrel. 27, Created)	
DT	05-JUN-2004	(TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	Outer membrane protein II (Fragment).		
GN	Name=OmpA;		
OS	Klebsiella oxytoca.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		
OC	Enterobacteriaceae; Klebsiella.		
NCBI_TaxID=571;			
[1]			
RN	SEQUENCE FROM N.A.		
RP			

RA	Wertz J.E., Goldstone C., Gordon D.M., Riley M.A.;
RT	"A molecular phylogeny of enteric bacteria and implications for a
FT	bacterial species concept.";
CC	J. Evol. Biol. 16:1236-1248(2003).
CC	-I- SIMILARITY: Belongs to the ompA family.
DR	EWBL; AV301193; AAO96087.1; -.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR	GO; GO:0005198; F:structural molecule activity; IEA.
DR	InterPro; IPR008664; Bac_OmpA.
DR	InterPro; IPR002368; OmpA.
DR	InterPro; IPR006665; OmpA/MotB.
DR	InterPro; IPR000498; OmpA_tmem.
DR	Pfam; PF00691; OmpA; 1.
DR	Pfam; PF01389; OmpA membrane; 1.
DR	PRINTS; PR01021; OMPADQMAMN.
DR	PRINTS; PR01022; OUTRMMBRANEA.
DR	ProDom; PD000930; OmpA/MotB; 1.
FT	NON TER 1
FT	NON TER 162
SQ	SEQUENCE 162 AA; 17469 MW; B5B532F2BCBF0C52 CRC64;

	Query Match	45.8%	Score 835;	DB 2;	Length 162;
	Best Local Similarity	97.5%;	Pred. No. 2.2e-56;		
	Matches 150;	Conservative 2;	Mismatches 2;	Indels 0;	Gaps 0
Qy	103	DDLDIYTRLGGMWRADSKNGYASTGVSRSSEHDTGVSVPFAGGVEMAVTRDIATRLRYQW	162		
Db	1	DDLDIYTRLGGMWRADSKNGYASTGVSRSSEHDTGVSVPFAGGVEMAVTRDIATRLRYQW	60		
Qy	163	VNNIGDAGTGTGTRPDNGMLSLGYSYRFGQEDAAPVAPAPAPAEVATKHTFLKSDVLFN	222		
Db	61	VNNIGDAGTGTGTRPDNGMLSLGYSYRFGQEDVAPVAPAPAPAEVTTKHTFLKSDVLFN	120		
Qy	223	FNKATLKPEQGOALDQLYTQISNNMDPKDGSANVLGYTDRIGS	264		
Db	121	FNKSTLKPEQGOALDQLYTQISNNMDPKDGSANVLGYTDRIGS	162		

RESULT 38	
Q6WAG1	
ID	PRELIMINARY; PRT; 162 AA.
AC	Q6WAG1
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE	Outer membrane protein II (Fragment).
GN	Name=ompA;
OS	Klebsiella oxytoca.

OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Klebsiella.
OX	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=MISC499;
RC	MEDLINE=33001863; PubMed=14640415;
RA	Wertz J.E., Goldstone C., Gordon D.M., Riley M.A.;
RX	"A molecular phylogeny of enteric bacteria and implications for a
RT	bacterial species concept.";
RT	J. Evol. Biol. 16:1236-1248(2003).
RL	-I- SIMILARITY: Belongs to the ompA family.
CC	EMBL; AY301192; AAQ96086.1; --
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR	GO; GO:0005198; F:structural molecule activity; IEA.
DR	InterPro; IPR006664; Bac OmpA.
DR	InterPro; IPR002368; OmpA.
DR	InterPro; IPR006665; OmpA/MotB.
DR	InterPro; IPR000498; OmpA_tmtn.
DR	Pfam; PF01691; OmpA; 1.
DR	Pfam; PF01389; OmpA membrane; 1.
DR	PRINTS; PR01021; OMPADOMAIN.
DR	PRINTS; PR01022; OUTRMMERANEA.
DR	PRODOM; PD000930; OmpA/MotB; 1.
FT	NON_TER 1
FT	NON_TER 162
FT	NON_TER 162
SQ	SEQUENCE 162 AA; 17469 MW; B5B532F2BCBF0C52 CRC64;
Query Match 45.8%; Score 835; DB 2; Length 162;	
Best Local Similarity 97.5%; Pred.No. 2.2e-56;	
Matches 158; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	
QY	103 DDLDIVYTRLGGVMWRADSKGNVYSTGVSRSEHDTGVSPPVAGGVEAVTRDIATRLFYOW 162
Db	1 DDLDIVYTRLGGVMWRADSKGNVYSTGVSRSEHDTGVSPPVAGGVEAVTRDIATRLFYOW 60
QY	163 VNNIGDAGTVGTRPDNGMLSLGVSYRFQGEDAAPVPAPAPAPAEVATKHTLKSDVLFN 222
Db	61 VNNIGDAGTVGTRPDNGMLSLGVSYRFQGEDVAPVPAPAPAEVITKHTLKSDVLFN 120
QY	223 FNKATLKPEQQALDQLYTOLSNMDDPKGS AVLGYTDRIQS 264
Db	121 FNKSTLKPEQQALDQLYTOLSNMDDPKGS AVLGYTDRIQS 162
RESULT 39	
Q6WAG2	PRELIMINARY; PRT; 162 AA.
ID Q6WAG2 AC Q6WAG2:	
DT 05-JUL-2004 (TREMBlrel. 27, Created)	
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)	
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)	
DE Outer membrane protein II (Fragment).	
GN Name=ompA;	
OS Klebsiella oxytoca.	
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
OC Enterobacteriaceae; Klebsiella.	
OX [1]	
RN	SEQUENCE FROM N.A.
RP	STRAIN=MISC192;
RC	MEDLINE=33001863; PubMed=14640415;
RA	Wertz J.E., Goldstone C., Gordon D.M., Riley M.A.;
RX	"A molecular phylogeny of enteric bacteria and implications for a
RT	bacterial species concept.";
RT	J. Evol. Biol. 16:1236-1248(2003).
RL	-I- SIMILARITY: Belongs to the ompA family.
CC	EMBL; AY301191; AAQ96085.1; --
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR	GO; GO:0005198; F:structural molecule activity; IEA.
DR	InterPro; IPR006664; Bac OmpA.


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RESULT 44
OS1841
ID OS1841 PRELIMINARY; PRT; 346 AA.
AC OS1841;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Outer membrane protein 34 precursor.
GN Name=omp34;
OS Actinobacillus actinomycetemcomitans (Haemophilus
OC actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OC NCBI_TaxID=714;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=NCCT 9710;
RA MEDLINE=98084499; PubMed=9423883;
RX White P.A., Nair S.P., Kim M.J., Wilson M., Henderson B.:
RT "Molecular characterization of an outer membrane protein of
RT Actinobacillus actinomycetemcomitans belonging to the OmpA family." ;
RL Infect. Immun. 66:369-372(1998).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; AF005079; AAC00068.1; -.
DR PIR; A60336; A60336.
DR HSP; P02934; 1BXW.
DR GO; GO:0015021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria) ; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.

```

Db 56 VNNIGDNTGVGVPDNGMLSGVSYRFGQEDAAPIVAPAPAPAEVQTKHFTLKSDVLF 115
 Qy 222 NFNKATLKPEGQALDQLYTQLSNMDPKDGSVVGLGYTDRIGS 264
 Db 116 NFNKATLKPEGQALDQLYTQLSNLDPKDGSSVVVLGFTDRIGS 158

RESULT 47
 Q6WAH9
 ID Q6WAH8 PRELIMINARY; PRT; 158 AA.
 AC Q6WAH8; 2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Outer membrane protein II (Fragment).
 GN Name=ompA;
 OS Enterobacter cloacae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Enterobacter.
 NCBI_TaxID=550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISC99;
 RX MEDLINE=23001863; PubMed=1460415;
 RT Wertz J.E., Goldstone C., Gordon D.M., Riley M.A.;
 RA "A molecular phylogeny of enteric bacteria and implications for a
 RL bacterial species concept."
 RJ J. Evol. Biol. 16:1236-1248(2003).
 CC -I- SIMILARITY: Belongs to the ompA family.
 DR EMBL; AY301175; AAQ96069.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR006664; BacOmpA.
 DR InterPro; IPR002368; OmpA.
 DR InterPro; IPR006665; OmpA/MotB.
 DR InterPro; IPR000498; OmpA_tmam.
 DR Pfam; PF00691; OmpA; 1.
 DR Pfam; PF01389; OmpA membrane; 1.
 DR PRINTS; PR01021; OMPADOMAIN.
 DR PRINTS; PR01022; OUTRMWBRANEA.
 DR ProDom; PD000930; OmpA/MotB; 1.
 FT NON_TER 1
 FT NON_TER 158 158
 SQ SEQUENCE 158 AA; 17042 MW; D72EA041B7B367BF CRC64;

Query Match 40.1%; Score 730; DB 2; Length 158;
 Best Local Similarity 85.3%; Pred. No. 2.6e-48;
 Matches 139; Conservative 9; Mismatches 9; Indels 6; Gaps 2

Qy 103 DLDLDIVYTRLGGVWVRADSKGNVYASTGVSREHDTGSPVFAAGGVWAVTRDIATRLQYOW 162
 Db 1 DLDLDIVYTRLGGVWVRADSKGNVYASTGVSREHDTGSPVFAAGGVWAVTRDIATRLQYOW 55

Qy 163 VNNIGDAGTVGTRPDNGMLSLGVSYRFG-QEDAAPVVPAPAPAPAEVATKHFTLKSDVLF 221
 Db 56 VNNIGDNTGVGVPDNGMLSGVSYRFGQEDAAPIVAPAPAPAEVQTKHFTLKSDVLF 115

Qy 222 NFNKATLKPEGQALDQLYTQLSNMDPKDGSVVGLGYTDRIGS 264
 Db 116 NFNKATLKPEGQALDQLYTQLSNLDPKDGSSVVVLGFTDRIGS 158

RESULT 48
 Q6WAH9
 ID Q6WAH9 PRELIMINARY; PRT; 158 AA.
 AC Q6WAH9;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Outer membrane protein II (Fragment).
 GN Name=ompA;

Qy	1	MKAIFVLNAAAPKONTWTYAGGKLGWSQYHD-----TGfYNGNQNNNGPTRNDQ	48
Db	13	LAASVAQAAPQNTFTVGAAGWASPHDGLNQAKYLEAPEATF---GFKENS-----	62
Qy	49	LGAGAGGQYQNPYLGFEMGYDWLG-----RMAYIGSVNDGAFK--AQGVOLTAKLGYPT	102
Db	63	VTVGVFGYQITONFAVELGYDFFGRAKLRMAEKDQKAKDAAKTTHGAHLSLKASYPYL	122
Qy	103	DLDDIYTRLGGMVWRADSK---GNVASTGVSRSSEHDTGVSPVFAGGVEMAVTRDIA	158
Db	123	DGLDIYARVGAALIRSYKYVDHSDPAKLPOFKRTHSTQVSPVFAGGUEYAFMPEALURV	182
Qy	159	EYQVNNNIGD-----ACTVGTTRPDNGMLSLGVSRYFGQEDAAPVVAPAPAPAEVATKHF	213
Db	183	EYQVNNNVGKVDLGERVDYRDPDIGSVTAGLSYRFGQS-----VVVPEVVSKTF	232
Qy	214	TLKSDVLFPNFKATLRPEGQALDQLYTQLSNMDDPKGSAAVVLGYTDRIGSEAYNQQLSE	273
Db	233	TLNSDVTFFGDKADLPKAAQNVLDGITYGEIAQL--KSASVAVAGYTRDLGSDAYNLKLSQ	290
Qy	274	KRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVK	333
Db	291	RRADTVANYLVAKGVAQNALISAIGHGEANPVTGNKCDSVKGRKALLIACLADRRVEIAVK	350
Qy	334	GYK 336	
Db	351	GNK 353	
RESULT 52			
Q6GUB4	ID	Q6GUB4 PRELIMINARY; PRT; 353 AA.	
AC	DT	06-JUL-2004 (TrEMBLrel. 27, Created)	
DT	DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT	DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE	DE	OmpA.	
OS	OS	Pasteurella multocida.	
OC	OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;	
OC	OC	Pasteurellaceae; Pasteurella.	
OX	NCBI_TaxID=747;		
RN	[1]	SEQUENCE FROM N.A.	
RC	RC	STRAIN=T94289;	
RA	RA	Akridge H., Confer A.W., Dabo S.M.;	
RL	RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	
CC	-1-	SIMILARITY: Belongs to the ompA family.	
DR	GO;	EMBL; AY643798; AAT57680.1; -.	
DR	GO;	GO:0016021; C:integral to membrane; IEA.	
DR	GO;	GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.	
DR	GO;	GO:0005198; F:structural molecule activity; IEA.	
DR	InterPro;	IPR006664; BacOmpA.	
DR	InterPro;	IPR002368; OmpA.	
DR	InterPro;	IPR006665; OmpA/MotB.	
DR	InterPro;	IPR006690; OMPA LIKE.	
DR	InterPro;	IPR000498; OmpA_tmam.	
DR	Pfam;	PF00691; OmpA; 1.	
DR	Pfam;	PF01389; OmpA membrane; 1.	
DR	PRINTS;	PR01021; OMPADOMAIN.	
DR	PRINTS;	PR01022; OUTRMEMBRANE.	
DR	ProDom;	PD000930; OmpA/MotB; 1.	
DR	PROSITE;	PS01068; OMPA; 1.	
DR	SEQUENCE	353 AA; 37964 MW; 1B1399FC2B27DBA CRC64;	
Query Match 39.8%; Score 724.5; DB 2; Length 353;			
Best Local Similarity 44.4%; Pred. No. 1.9e-47;			
Matches .157; Conservative 48; Mismatches 118; Indels 31; Gaps 7			
Qy	1	MKAIFVLNAAAPKONTWTYAGGKLGWSQYHD-----GSVDNGAFKAQGVOLTAKLGYPTDDDDIYTRL	57
Db	13	LAASVAQAAPQNTFTVGAAGWASPHDGLNQAKYLEAPEATF---GFKENS-----	71
Qy	58	QNPYLGFEMGYDWLGRWAYK-----GSVDNGAFKAQGVOLTAKLGYPTDDDDIYTRL	111

DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBERNEA.
DR ProDom; PD000930; OmpA/MotB; 1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 16929 MW; 3AFC4F08B6316144 CRC64;

Query Match 39.1%; Score 712.5; DB 2; Length 157;
Best Local Similarity 84.6%; Pred. No. 5.7e-47;
Matches 137; Conservative

Qy 103 DDLDDIYTRLGGMVWRADSKGNVASTGVSRSEHDTGVSVPFAGGVWAVTRDIATRLRYQM 162
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 1 DDLDIYTRLGGMVWRADTKSN-----VYGKNDHTGVSVPFAGGVAYITPEIATRLRYQM 55
| | | | | | | | | | | | | | | | | | | | | | : | | | | |

Qy 163 VNNIGDAGTVGTRPDNGMLSLGSVSRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFN 222
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 56 TNNIGDAHTIGTRPDNGMLSLGSVSRFGGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFN 115
| | | | | | | | | | | | | | | | | | | | | | : | | | | |

Qy 223 FNKATLKPEGQAALDOLYTQLNSMDPKDGSAAVVLGYTDRIGS 264
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 116 FNKATLKPEGQAALDOLYSQLSLNLPDKGSGVVVLGYTDRIGS 157
| | | | | | | | | | | | | | | | | | | | | | : | | | | |

RESULT 58
ID Q6WAH2 PRELIMINARY; PRT; 157 AA.

AC Q6WAH2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Outer membrane protein II (Fragment).
GN Name=ompA;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TA57;
RX MEDLINE=23001863; PubMed=14640415;
RA Wertz J.E., Goldstone C., Gordon D.M., Riley M.A.;
RT "A molecular phylogeny of enteric bacteria and implications for a
bacterial species concept."
J. Evol. Biol. 16:1236-1248(2003).
CC -|- SIMILARITY: Belongs to the ompA family.
DR EMBL; AY301181; AAQ96074.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_tmcm.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBERNEA.
DR ProDom; PD000930; OmpA/MotB; 1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 16929 MW; 3AFC4F08B6316144 CRC64;

Query Match 39.1%; Score 712.5; DB 2; Length 157;
Best Local Similarity 84.6%; Pred. No. 5.7e-47;
Matches 137; Conservative

Qy 103 DDLDDIYTRLGGMVWRADSKGNVASTGVSRSEHDTGVSVPFAGGVWAVTRDIATRLRYQM 162
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 1 DDLDIYTRLGGMVWRADTKSN-----VYGKNDHTGVSVPFAGGVAYITPEIATRLRYQM 55
| | | | | | | | | | | | | | | | | | | | | | : | | | | |

Qy 163 VNNIGDAGTVGTRPDNGMLSLGSVSRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFN 222
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 56 TNNIGDAHTIGTRPDNGMLSLGSVSRFGGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFN 115
| | | | | | | | | | | | | | | | | | | | | | : | | | | |

Qy 223 FNKATLKPEGQAALDOLYTQLNSMDPKDGSAAVVLGYTDRIGS 264
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 116 FNKATLKPEGQAALDOLYSQLSLNLPDKGSGVVVLGYTDRIGS 157
| | | | | | | | | | | | | | | | | | | | | | : | | | | |

RESULT 58
ID Q6WAH2 PRELIMINARY; PRT; 157 AA.

AC Q6WAH2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Outer membrane protein II (Fragment).
GN Name=ompA;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TA57;
RX MEDLINE=23001863; PubMed=14640415;
RA Wertz J.E., Goldstone C., Gordon D.M., Riley M.A.;
RT "A molecular phylogeny of enteric bacteria and implications for a
bacterial species concept."
J. Evol. Biol. 16:1236-1248(2003).
CC -|- SIMILARITY: Belongs to the ompA family.
DR EMBL; AY301181; AAQ96075.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_tmcm.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBERNEA.
DR ProDom; PD000930; OmpA/MotB; 1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 16929 MW; 3AFC4F08B6316144 CRC64;

Query Match 39.1%; Score 712.5; DB 2; Length 157;
Best Local Similarity 84.6%; Pred. No. 5.7e-47;
Matches 137; Conservative

Qy 103 DDLDDIYTRLGGMVWRADSKGNVASTGVSRSEHDTGVSVPFAGGVWAVTRDIATRLRYQM 162
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 1 DDLDIYTRLGGMVWRADTKSN-----VYGKNDHTGVSVPFAGGVAYITPEIATRLRYQM 55
| | | | | | | | | | | | | | | | | | | | | | : | | | | |

Qy 163 VNNIGDAGTVGTRPDNGMLSLGSVSRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFN 222
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 56 TNNIGDAHTIGTRPDNGMLSLGSVSRFGGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFN 115
| | | | | | | | | | | | | | | | | | | | | | : | | | | |

Qy 223 FNKATLKPEGQAALDOLYTQLNSMDPKDGSAAVVLGYTDRIGS 264
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 116 FNKATLKPEGQAALDOLYSQLSLNLPDKGSGVVVLGYTDRIGS 157
| | | | | | | | | | | | | | | | | | | | | | : | | | | |

RESULT 60
ID Q6WAHS PRELIMINARY; PRT; 157 AA.

AC Q6WAHS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Outer membrane protein II (Fragment).
GN Name=ompA;
OS Escherichia coli.

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Escherichia.
 [1]
 NCBI_TaxID=562;
 RN SEQUENCE FROM N.A.
 RC STRAIN=TAL57;
 RX MEDLINE=3001863; PubMed=1460415;
 RA Wertz J.E., Goldstone C., Gordon D.M., Riley M.A.;
 RT "A molecular phylogeny of enteric bacteria and implications for a
 bacterial species concept.";
 RL J. Evol. Biol. 16:1236-1248(2003).
 CC -1. SIMILARITY: Belongs to the ompA family.
 DR EMBL; AY3011178; AAQ96072.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0002979; C: outer membrane (sensu Gram-negative Bacteria); IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR006664; Bac OmpA.
 DR InterPro; IPR002368; OmpA.
 DR InterPro; IPR008665; OmpA/MotB.
 DR InterPro; IPR000498; OmpA_tmern.
 DR Pfam; PF00691; OmpA; 1.
 DR PRINTS; PR01389; OmpA membrane; 1.
 DR PRINTS; PR01021; OMPADOMAIN.
 DR PRINTS; PR01022; OUTRAMBRANEA.
 DR ProDom; PD000930; OmpA/MotB; 1.
 FT NON TER 1
 FT NON TER 157 157
 SQ SEQUENCE 157 AA; 16929 MW; 3AFC4F08B6316144 CRC64;
 Query Match 39.1%; Score 712.5; DB 2; Length 157;
 Best Local Similarity 84.6%; Pred. No. 5.7e-47;
 Matches 137; Conservative 8; Mismatches 12; Indels 5; Gaps 1;
 QY 103 DDLDIYTRLGGVWVRADSKNYASTGVSRSRSHDTGVSVPFAGGVWAVTRDIATRLVYQW 162
 DB 1 DDLDIYTRLGGVWVRADTKSN-----VYGRKNDTGVSVPFAGGVYAITPIATRLVYQW 55
 QY 163 VNNIGDAGTVGTRPDNGMLSLGVSRYRFGQEDAAPVWAPAPAPAEVATKHFTHKSDVLFN 222
 DB 56 TNNIGDAHTIGTRPDNGMLSLGVSRYRFGQGAAPVWAPAPAPAEVQTKHFTHKSDVLFN 115
 QY 223 FNKATLKPEGQAALDQLYTQLSNMDDPKDGSAVVLGYTDRIQS 264
 DB 116 FNKATLKPEGQAALDQLYSQLSNLDPKDGVSVVVLGYTDRIQS 157
 RESULT 61
 ID Q8VPL3 PRELIMINARY; PRT; 348 AA.
 AC Q8VPL3;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE OmpA.
 GN Name=OmpA;
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Pasteurella.
 OC NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=232;
 RX MEDLINE=22048590; PubMed=12052333; DOI=10.1016/S0378-1135(02)00068-8;
 RA Gatto N.T., Dabo S.M., Hancock R.E., Confer A.W.;
 RT "Characterization of, and immune responses of mice to, the purified
 OmpA-equivalent outer membrane protein of Pasteurella multocida
 serotype A:3 (Omp28).";
 RL Vet. Microbiol. 87:221-235(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=232;
 RA Dabo M.S., Confer A.W.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; CmpA membrane; 1.
DR PRINTS; PRO1021; OMPADOMAIN.
DR PRINTS; PRO1022; OUTRMWBRANE.
DR ProDom; PD000930; OmpA/MotB; 1.
SQ SEQUENCE 364 AA; 38662 MW; 83D13B28DAFF6D46 CRC64;

Query Match 38.2%; Score 696.5; DB 2; Length 364;
Best Local Similarity 42.5%; Pred.No.2.9e-45;
Matches 152; Conservative 60; Mismatches 115; Indels 31; Gaps 9;

Qy 3 AIFVLNAAPKDNFTYAGGKLGSVQH-----TGFYGNGFQNNGPT----RNDQLGAGA 53
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 14 AVASANAPEANSFYVGAKAGATPHHGVNQFNPKSVANDERYSDGPATAYGINRNSTVTGV 73

Qy 54 FGYYQNVPYLGEFGMDWLGRMAYKGSVDNGAFL--AQGVLTAKLGYPIITDDLDIYTR 110
 || || || || || || || || || || || || || || || || || || || || || || ||
Db 74 FGGYQIIDNLAVELGDYDFGRV--RGNVGDRRAFDTKHGAIHSIKPSYEVSGLDLGYK 131

Qy 111 LCGMWWRADS KGNYSTGVSRSEHDGTGSPFAGGVWEAWTVTDIAIRLEYOWNNIGDAG 170
 || || || || || || || || || || || || || || || || || || || || || || ||
Db 132 VQAALVRNDYKDYYAN-GTYDKSHLNKTSLILGAGVEVAITPALAAVRLEYOQLSRAGNYG 190

Qy 171 TVGTR-----PDNGMLSLGVSYRFQGDDAAPVVAPA PAPAPEVATKHFTLKSDVL 220
 :
Db 191 KAERKAGNVTDLRYSPDAHVSAGLYTFREGQ-AAAPVVA---EPEIVTNKFASFSSDVL 244

Qy 221 FNFKKATLPBGQQALDQLYTOLSNMPPKGSAVVLGYTDRLGSGAYNQOISEKRAQSIV 280
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 245 FDPGKANLPAAAASJDAHAIEIONGLAIPAIOVNGYTDRIGDKDPNALLSORAEBSVA 304

Qy 281 DYLVAKGIIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPPRRVEIEVKGYKEV 338
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 305 NYMVSKGVAPESTITAVGYGKAMPVTGNTCDAVKRKALIACLA PRRVELQVQGSKEV 362

RESULT 63

O6PSKS PRELIMINARY; PRT; 364 AA.

ID Q6PSKS AC Q6PSK5 AT Q6PSK5 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pastereullaceae; Pasteurella.
OX NCBI_TaxID=47735;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=PH246, and PH68;
RX PubMed=15317779; DOI=10.1128/J.B.186.17.5741-5752.2004;
RV Davies R.L., Lee J.;
RA "Sequence diversity and molecular evolution of the heat-modifiable outer membrane protein gene (ompA) of Mannheimia (Pasteurella) haemolytica, Mannheimia glucosida, and Pasteurella trehalosi.";
RL J. Bacteriol. 186(5):5741-5752(2004).
CC -I- SIMILARITY: Belongs to the ompA family.
DB EMBL; AY582756; AAC91721.1; --
DR EMBL; AY582755; AAC91717.1; --
GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac.OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_tmem.
PFam; PF00691; OmpA; 1.
PRINTS; PRO1021; OMPADOMAIN.
OUTRMWBRANE.
PRO1022;
PROMODIN.
PROMODIN; PD000930; OmpA/MotB; 1.
SEQUENCE 364 AA; 38662 MW; 8AAGE91FB92ECAAF6 CRC64;

Matches 153; Conservative 46; Mismatches 124; Indels 18; Gaps 7;

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QY 1 MKAIFVLAAPKNDNTWYAGKLGWQYHDTGYGNGFQNNNGPTRNDOLGAGAFGGYQVN 60
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 13 LTAASVAQAAPQANTFYAGAKAGWASFDHGLNQFNSQADGTLN-SVTYGVFGYQIT 71

QY 61 PYLFEMGYDMLGRMAYK-GSVNDGAFKAQGVQLTAKLGYPTDLDLDIYTRLGGMVWRAD 119
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 72 DNFAVELGYDDFGRAKRRQGGTIVKYNHGAHLSLKASYPVLEGDLYVARVGAALIRSD 131

QY 120 SKGNVASTGVSRSSEHDTGVSVPFAGGVWAVTR--DIATRLLEYQWVNNIG----DAGTVG 173
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 132 YKPTRAAPNQTHSHSLKVSVPFAGGLEYNLPSLPALRVEYQWVNVKVRKDGSRVD 191

QY 174 TRPDNGMLSLGVSYRFGQEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 233
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 192 YTPSIGSVTAGLSYRFGQ--SAPVV-----EPKVAKTFALNSDVTFAFGKANLRPEAQ 243

QY 234 QALDOLYTLQSNMPPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKI 293
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 NVLDGIYGEIAQL--KSVQVDVAGYTDRIQSEAAANLKLSSRRADTVANVLSKGVQAEVI 301

QY 294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 302 SSTGYGEANPVTGAKCDTVKGRKALIACLADRRRVEISVKG 342

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RESULT 65

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Q8RMW1 PRELIMINARY; PRT; 344 AA.
AC Q8RMW1;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hemagglutinin antigen.
GN Name=haga;
OS Haemophilus gallinarum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Avibacterium.
OX NCBI_TaxID=728;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=0222;
RX MEDLINE=22095958; PubMed=12101304;
RA Hobb R.I., Tseng H.-J., Downes J.E., Terry T.D., Blackall P.J.,
RA Takagi M., Jennings M.P.;
RT "Molecular analysis of a haemagglutinin of Haemophilus
paragallinarum.";
RL Microbiology 148:2171-2179(2002).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; AF491819; AAM00927.1; -.
DR HSSP; P02934; 1QJP.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRODOM; PD000930; OmpA/MotB; 1.
DR SEQUENCE 344 AA; 36788 MW; 8E31491FB3E8CAF6 CRC64;

```

Query Match 37.8%; Score 688; DB 2; Length 344;

Best Local Similarity 44.9%; Pred. No. 1.2e-44;

Matches 153; Conservative 46; Mismatches 124; Indels 18; Gaps 7;

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QY 1 MKAIFVLAAPKNDNTWYAGKLGWQYHDTGYGNGFQNNNGPTRNDOLGAGAFGGYQVN 60
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 13 LTAASVAQAAPQANTFYAGAKAGWASFDHGLNQFNSQADGTLN-SVTYGVFGYQIT 71

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```

QY 61 PYLFEMGYDMLGRMAYK-GSVNDGAFKAQGVQLTAKLGYPTDLDLDIYTRLGGMVWRAD 119
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 72 DNFAVELGYDDFGRAKRRQGGTIVKYNHGAHLSLKASYPVLEGDLYVARVGAALIRSD 131

QY 120 SKGNVASTGVSRSSEHDTGVSVPFAGGVWAVTR--DIATRLLEYQWVNNIG----DAGTVG 173
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 132 YKPTRAAPNQTHSHSLKVSVPFAGGLEYNLPSLPALRVEYQWVNVKVRKDGSRVD 191

QY 174 TRPDNGMLSLGVSYRFGQEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 233
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 192 YTPSIGSVTAGLSYRFGQ--SAPVV-----EPKVAKTFALNSDVTFAFGKANLRPEAQ 243

QY 234 QALDOLYTLQSNMPPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKI 293
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 NVLDGIYGEIAQL--KSVQVDVAGYTDRIQSEAAANLKLSSRRADTVANVLSKGVQAEVI 301

QY 294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 302 SSTGYGEANPVTGAKCDTVKGRKALIACLADRRRVEISVKG 342

```

RESULT 66

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Q6GUB8 PRELIMINARY; PRT; 349 AA.
AC Q6GUB8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE OmpA.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95010872;
RA Akridge H., Confer A.W., Dabo S.M.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; AY643794; AAT57676.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR006690; OmpA_LIKE.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMRANE.
DR PRODOM; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OmpA; 1.
DR SEQUENCE 349 AA; 37639 MW; 68E96F7EBAB47DC1 CRC64;

```

Query Match 37.7%; Score 586.5; DB 2; Length 349;

Best Local Similarity 44.1%; Pred. No. 1.6e-44;

Matches 158; Conservative 41; Mismatches 106; Indels 53; Gaps 10;

```

QY 6 VLNAAPKNDNTWYAGKLGWQYHDTGYGNGFQNNNGPTRNDOLGAGA 53
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 VAQAAPQNTFYAGAKAGWASFDHGLNQAKYLEAPEATF---GPKRNS-----VTYGV 67

QY 54 FGGYQVNPYLGFMGYDWLG----RMAKGSVDNGAFK--AQGVQLTAKLGYPTDLDI 107
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 FGEYQITDNFAVELGYDDFGRAKLMAEKDKAKDAKHTNHGAHLSLKASYPVLGLDI 127

QY 108 YTRLGGMVWRADSK-----GNVASTGVSRSSEHDTGVSVPFAGGVWAVTRDIATRLLEYQWV 163
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 YARVGAALIRSDYKVDHSDPAKLQPKRTHSTQVSPVFAGGLEAYAFMPALRVEYQWV 187

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Db 192 YTPSIGSVTAGLSYRFGQ--SAPVV-----EPKVAKTFAINSDVTFAGKANLRPEAQ 243
Qy 234 QALDOLYTLQSNMPPKDGSAVVLGYTDRIQSEAYNQQLSEKRAQSVVDYLVAKGIPAGKI 293
Db 244 NVLDGIYGEIAQL--KSVQVDLAGYTDRIQSEAAANLKLSSRADTVANVYLVSKGVAQEV 301
Qy 294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVK 334
Db 302 SSTGYGEANPVTGAKCDVAKGRKALITACIADDRRVEISVK 342

RESULT 69
Q8RML8 PRELIMINARY; PRT; 344 AA.
AC Q8RML8;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hemagglutinin antigen.
GN Name=hagA;
OS Haemophilus gallinarum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Avibacterium.
OX NCBI_TaxID=728;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2671;
RX MEDLINE=22095958; PubMed=12101304;
RA Hobb R.I., Tseng H.-J., Downes J.E., Terry T.D., Blackall P.J.,
RA Takagi M., Jennings M.P.;
RT "Molecular analysis of a haemagglutinin of Haemophilus
paragallinarum.";
RL Microbiology 148:2171-2179 (2002).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; AF491822; AAM00930.1; -.
DR HSSP; P02934; 1BXW.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTERMERANE.
DR ProDom; PD000930; OmpA/MotB; 1.
SQ SEQUENCE 344 AA; 36762 MW; 2E3142AFB3E8CDF0 CRC64;

Query Match 37.5%; Score 684; DB 2; Length 344;
Best Local Similarity 44.9%; Pred. No. 2.4e-44;
Matches 153; Conservative 45; Mismatches 125; Indels 18; Gaps 7;

Qy 1 MKAIFVLNAAPKONTWYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDOLGAGAFGGYQVN 60
Db 13 LTAASVAQAAPQANTFYAGAKAGWASFDHGLNQFNSQNAQGLTRN-SVTYGVFGYQIT 71
Qy 61 PYLFGEMGYDNLGRMAYK-GSVNDGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWVRAD 119
Db 72 DNFAVELGYDDFGRAKLRRQGGETVIKHTNHGAHLSKASYPVLEGLDYYARVGAALIRSD 131
Qy 120 SKGNVASTGVSRSRSHDTGVSFVAGGVWAVTR--DIATRLGYQWANNIG----DAGTVG 173
Db 132 YKPTKRAAPNQTTHSLKSVFVAGGLEYNLPSPLEALRVEYQWNVKGVKDGSRVD 191
Qy 174 TRPDNGLSLGVSRYFGQDEAPVVAAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 233
Db 192 YTPSIGSVTAGLSYRFGQ--SAPVV-----EPKVAKTFAINSDVTFAGKANLRPEAQ 243
Qy 234 QALDOLYTLQSNMPPKDGSAVVLGYTDRIQSEAYNQQLSEKRAQSVVDYLVAKGIPAGKI 293
Db 244 NVLDGIYGEIAQL--KSVQVDLAGYTDRIQSEAAANLKLSSRADTVANVYLVSKGVAQEV 301
Qy 294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVK 334
Db 302 SSTGYGEANPVTGAKCDVAKGRKALITACIADDRRVEISVK 342

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```

Qy 294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVK 334
Db 302 SSTGYGEANPVTGAKCDVAKGRKALITACIADDRRVEISVK 342

RESULT 70
Q8RML8 PRELIMINARY; PRT; 344 AA.
AC Q8RML8;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hemagglutinin antigen.
GN Name=hagA;
OS Haemophilus gallinarum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Avibacterium.
OX NCBI_TaxID=728;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SA-3;
RX MEDLINE=22095958; PubMed=12101304;
RA Hobb R.I., Tseng H.-J., Downes J.E., Terry T.D., Blackall P.J.,
RA Takagi M., Jennings M.P.;
RT "Molecular analysis of a haemagglutinin of Haemophilus
paragallinarum.";
RL Microbiology 148:2171-2179 (2002).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; AF491824; AAM00932.1; -.
DR HSSP; P02934; 1BXW.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_tmern.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTERMERANE.
DR ProDom; PD000930; OmpA/MotB; 1.
SQ SEQUENCE 344 AA; 36868 MW; FD55FDB10109763B CRC64;

Query Match 37.5%; Score 683; DB 2; Length 344;
Best Local Similarity 44.6%; Pred. No. 2.9e-44;
Matches 152; Conservative 46; Mismatches 125; Indels 18; Gaps 7;

Qy 1 MKAIFVLNAAPKONTWYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDOLGAGAFGGYQVN 60
Db 13 LTAASVAQAAPQANTFYAGAKAGWASFDHGLNQFNSQNAQGLTRN-SVTYGVFGYQIT 71
Qy 61 PYLFGEMGYDNLGRMAYKGSVDN-GAPKAQGVQLTAKLGYPTDLDIYTRLGGMWVRAD 119
Db 72 DNFAVELGYDDFGRAKLRRQGGETVIKHTNHGAHLSKASYPVLEGLDYYARVGAALIRSD 131
Qy 120 SKGNVASTGVSRSRSHDTGVSFVAGGVWAVTR--DIATRLGYQWANNIG----DAGTVG 173
Db 132 YKPTKRAAPNQTTHSLKSVFVAGGLEYNLPSPLEALRVEYQWNVKGVKDGSRVD 191
Qy 174 TRPDNGLSLGVSRYFGQDEAPVVAAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 233
Db 192 YTPSIGSVTAGLSYRFGQ--SAPVV-----EPKVAKTFAINSDVTFAGKANLRPEAQ 243
Qy 234 QALDOLYTLQSNMPPKDGSAVVLGYTDRIQSEAYNQQLSEKRAQSVVDYLVAKGIPAGKI 293
Db 244 NVLDGIYGEIAQL--KSVQVDLAGYTDRIQSEAAANLKLSSRADTVANVYLVSKGVAQEV 301
Qy 294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVK 334
Db 302 SSTGYGEANPVTGAKCDVAKGRKALITACIADDRRVEISVK 342

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OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC	Pasteurellaceae; Avibacterium.
OX	NCBI_TaxID=728;
RP	[1]
RP	SEQUENCE FROM N.A.
RP	STRAIN-Sd-1;
RA	Deyuan M., Huiling S., Peijun Z., Yumei G.;
RL	Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RP	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Tianjin;
RA	Miao D., Sun H., Lu L., Pan Y., Gong Y., Zhan P.;
RL	Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC	-1- SIMILARITY: Belongs to the ompA family.
DR	EMBL; AY388647; AAQ86765.2; -.
DR	EMBL; AY622379; AAT40990.1; -.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR	GO; GO:0005198; F:structural molecule activity; IEA.
DR	InterPro; IPR006664; Bac_OmpA.
DR	InterPro; IPR002368; OmpA.
DR	InterPro; IPR006665; OmpA/MotB.
DR	InterPro; IPR000498; OmpA_tmam.
DR	Pfam; PF00691; OmpA; 1.
DR	Pfam; PF01389; OmpA membrane; 1.
DR	PRINTS; PR01021; OMPADOMAIN.
DR	PRINTS; PR01022; OUTRMMBRANE.
DR	ProDom; PD000930; OmpA/MotB; 1.
SQ	SEQUENCE 345 AA; 36925 MW; 61CDA42C873F763A CRC64;
Query Match 37.4%; Score 681.5; DB 2; Length 345;	
Best Local Similarity 45.4%; Pred. No. 3.8e-44;	
Matches 157; Conservative 43; Mismatches 119; Indels 27; Gaps 9	
Qy	1 MKAIFVLNAPKONTWYAGGKLGWSYHDTGTFYGNFGNNNGPTRNDOLGAGAFGGYOVN 60
Db	13 LTAASVAQAQAQNTFVAGAKAGWASPHDGLNQFENSQNAVGTURN-SVTYGVFGYQIT 71
Qy	61 PYLGFEMGYDWLGRMAY-KGSVDNGAFKAQGVQLTAKLGYPIITDLDIYTRLGGVMVRAD 119
Db	72 DNFAVELGYDDFGRKLKKGGETVIKHTNHGAHLSLKASYFVLSGLDVYARVGAALRSD 131
Qy	120 SKGNYASTGSVRS-----EHDGTGSPVPFAGVGVAVTR--DIATRLFYQWNNIG----D 168
Db	132 ----YKSTKRAESDYVMHEHSLKSPVPFAGGLEYNLPSELALRVEYQWNVKVRVEKD 187
Qy	169 AGTVGTRPDNGMLSLGVSYPFGDEAPVAVPAPAPAPAEVATKHFTLKSDDLNFNFKATL 228
Db	188 GSRVDYTPFSGSVTAGLSYRFQG--SAPW-----EPKVAKFTALMSDVTFAFGKANL 239
Qy	229 KPEQQALDQLYTOLSNNDPKDGSVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGI 288
Db	240 RPEAQNVLDGYIGIAQL--KSVQVDVAGYTDRIIGSEAAKLQRRADTVANYLVSKGV 297
Qy	289 PAGKISARGMGESNPVTGNTCDNVKARAALDCLAPRRRVEIEVKG 334
Db	298 AQEVISSGTGYEANPVTGAKCDVAKGRKALIACLADRRRVEISVKG 343
RESULT 73	
Q8RJ58	PRELIMINARY; PRT; 341 AA.
ID	Q8RJ58;
AC	Q8RJ58;
DT	01-JUN-2002 (TrEMBLrel. 21, Created)
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hemagglutinin antigen.
GN	Name=haga;
OS	Haemophilus gallinarum.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC	Pasteurellaceae; Avibacterium.
OX	NCBI_TaxID=728;
RP	[1]

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RP SEQUENCE FROM N.A.
RX STRAIN=HP60, HP14, and Modesto;
RC MEDLINE=22095958; PubMed=12101304;
RA Hobb R.I., Tseng H.-J., Downes J.E., Terry T.D., Blackall P.J.,
RA Takagi M., Jennings M.P.;
RT "Molecular analysis of a haemagglutinin of Haemophilus
paragallinarum.";
RL Microbiology 148:2171-2179(2002).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; AF491818; AA00926.1; -.
DR EMBL; AF491821; AA00929.1; -.
DR EMBL; AF491827; AA00935.1; -.
DR HSSP; P02934; IQDP.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBRANE.
DR ProDom; PD000930; OmpA/MotB; 1.
SQ SEQUENCE 341 AA; 36473 MW; 8CF6E5461CBA6D63 CRC64;

Query Match 37.3%; Score 680.5; DB 2; Length 341;
Best Local Similarity 44.7%; Pred. No. 4.5e-44;
Matches 151; Conservative 47; Mismatches 125; Indels 15; Gaps 7;

QY 1 MKAIFVLAAPKNDNTWYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQAGAGFGYQVN 60
Db 13 LTAASVAQAAPQANTFYAGAKAGWASFDGLNQFNSQNAVYGLRN-SVTVGVFGYQIT 71

QY 61 PYLGFEMGYDWMGRWYKGSVDNG-AFKAQGVQLTAKGYPTDDLDIYTRILGGMWTRAD 119
Db 72 DNFAVELGYDDFRGAKFRQDGETVTKHTNHGAHLSLKASYPVLEGLDYYARVGAALIRSD 131

QY 120 SKGNVASTGVSRSRSHDTGVSVPFAGGVWAVTR--DIATRLFYQWNNIG-DAGTVGTRP 176
Db 132 YKPTKRAAPNETHSHLSKSPVFAGGLEVNLSPLELALRVYQWNVKVRDGRSDVYTP 191

QY 177 DNGMLSLGVSRYFGQSDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 236
Db 192 SIGSVTAGLSYRFGQ--SAPVV-----EPKVAKTFALNSDVTFAFGKANLRPEAQNVL 243

QY 237 DQLYTQLSNMDPKDGSVAVLVGTDTRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISAR 296
Db 244 DGIYGEIAQL--KSVQVDLAGYTDTRIGSEAAVNLKLSQRRADTVANYLVSKGVAQEVISST 301

QY 297 GMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
Db 302 GYGEANPVTGAKCDVAKGRKALIACLADRRVEISVKG 339

RESULT 74
Q6WAI1 PRELIMINARY; PRT; 157 AA.
ID Q6WAI1
AC Q6WAI1;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Outer membrane protein II (Fragment).
GN Name=ompA;
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISC255;
RX MEDLINE=23001863; PubMed=14640415;

QY 1 DDLDIYTRILGGMVWRADSKGNVASTGVSRSRSHDTGVSVPFAGGVWAVTRDIATRLFYQW 162
Db 1 DDLDIYTRILGGMVWRADAKNN--TGF--KDHDTGVSVPFAGGVYATPEIATLELVQW 55

QY 163 VNNIGDAGTVGTRPDNGMLSLGVSRYRFG-QEDAAPVAPAPAPAPAPAPAPAPAPAPAPAP 221
Db 56 TNNIGDANTVGGTRPDNGMLLSVGVSRYRFGQSEAAFPVVV-ADAPAPEVQTKHFTLKSDVLF 114

QY 222 NFNKATLKPEGQOALDQLYTQLSNMDPKDGSVAVLVGTDTRIGS 264
Db 115 NFNKATLKPEGQOALDQMYSQLSNLDPKDGSVVVLGFTDTRIGS 157

RESULT 75
Q6WAI5 PRELIMINARY; PRT; 157 AA.
ID Q6WAI5
AC Q6WAI5;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Outer membrane protein II (Fragment).
GN Name=ompA;
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISC250;
RX MEDLINE=23001863; PubMed=14640415;
RA Wertz J.E., Goldstone C., Gordon D.M., Riley M.A.;
RT "A molecular phylogeny of enteric bacteria and implications for a
bacterial species concept.";
RL J. Evol. Biol. 16:1236-1248(2003).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; AY301172; AAQ96066.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBRANE.
DR ProDom; PD000930; OmpA/MotB; 1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 16976 MW; 4AC30255347BE115 CRC64;

Query Match 37.2%; Score 678.5; DB 2; Length 157;
Best Local Similarity 81.6%; Pred. No. 2.3e-44;
Matches 133; Conservative 13; Mismatches 10; Indels 7; Gaps 4;
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QY 103 DDLDIYTRILGGMVWRADSKGNVASTGVSRSRSHDTGVSVPFAGGVWAVTRDIATRLFYQW 162
Db 1 DDLDIYTRILGGMVWRADAKNN--TGF--KDHDTGVSVPFAGGVYATPEIATLELVQW 55

QY 163 VNNIGDAGTVGTRPDNGMLSLGVSRYRFG-QEDAAPVAPAPAPAPAPAPAPAPAPAPAPAP 221
Db 56 TNNIGDANTVGGTRPDNGMLLSVGVSRYRFGQSEAAFPVVV-ADAPAPEVQTKHFTLKSDVLF 114

QY 222 NFNKATLKPEGQOALDQLYTQLSNMDPKDGSVAVLVGTDTRIGS 264
Db 115 NFNKATLKPEGQOALDQMYSQLSNLDPKDGSVVVLGFTDTRIGS 157

RESULT 75
Q6WAI5 PRELIMINARY; PRT; 157 AA.
ID Q6WAI5
AC Q6WAI5;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Outer membrane protein II (Fragment).
GN Name=ompA;
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISC250;
RX MEDLINE=23001863; PubMed=14640415;
RA Wertz J.E., Goldstone C., Gordon D.M., Riley M.A.;
RT "A molecular phylogeny of enteric bacteria and implications for a
bacterial species concept.";
RL J. Evol. Biol. 16:1236-1248(2003).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; AY301168; AAQ96062.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBRANE.
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DR	ProDom; PD000930; OmpA/MotB; 1.
FT	NON_TER 1
FT	NON_TER 157
FT	NON_TER 157
SEQ	SEQUENCE 157 AA; 16976 MW; 4AC30255347B6115 CRC64;
Query Match 37.2%; Score 678.5; DB 2; Length 157;	
Best Local Similarity 81.6%; Pred. NO. 2.3e-44;	
Matches 133; Conservative 13; Mismatches 10; Indels 7; Gaps 4;	
Qy	103 DLDLIYTRLGGWVRADSKGNVASTGVSRSRSHDTGVSVPFAGGVAVTRDIATRLLEYQW 162
Db	1 DLDLVYTRLGGWVRADAKNN--TGF--KDHDTGVSVPFAGGVYAITPIATRLLEYQW 55
Qy	163 VNNIGDAGTGTTRPDNGLSLGVSYRFG-QBDAAPVVPAPAPAPAPEVATKHFTLKSDVLF 221
Db	56 TNNIGDANTVGGRPDNGLLSGVSYRFGQBEAAPVVV-APAPAPEVQTKHFTLKSDVLF 114
Qy	222 NFNKATLKPEGQQALDOLYTOLSNMDDKGSAGVLGYTDRIGS 264
Db	115 NFNKATLKPEGQQALDDQMYSQLNDDPKDGSVVVLGFTDRIGS 157
RESULT 76	
Q6WA12	PRELIMINARY; PRT; 157 AA.
ID	Q6WA12
AC	Q6WA12; ID
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Outer membrane protein II (Fragment).
GN	Name=ompA;
OS	Citrobacter freundii.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Citrobacter.
OX	NCBI_TaxID=546;
RX	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MISC140;
RC	MEDLINE=32001863; PubMed=14640415;
RA	Wertz J.E., Goldstone C., Gordon D.M., Riley M.A.;
RT	"A molecular phylogeny of enteric bacteria and implications for a
RT	bacterial species concept.";
RL	J. Evol. Biol. 16:1236-1248(2003).
CC	-1- SIMILARITY: Belongs to the ompA family.
DR	EWBL; AY301171; AAQ96085.1; -.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR	GO; GO:0005198; F:structural molecule activity; IEA.
DR	InterPro; IPR006664; Bac OmpA.
DR	InterPro; IPR002368; OmpA.
DR	InterPro; IPR006665; OmpA/MotB.
DR	InterPro; IPR000498; OmpA_tmem.
DR	Pfam; PF010691; OmpA; 1.
DR	Pfam; PF01389; OmpA membrane; 1.
DR	PRINTS; PR01021; OMPADOMAIN.
DR	PRINTS; PR01022; OUTRMVBRANEA.
DR	ProDom; PD000930; OmpA/MotB; 1.
FT	NON_TER 1
FT	NON_TER 157
FT	NON_TER 157
SEQ	SEQUENCE 157 AA; 17004 MW; A3A61755346B741A CRC64;

Qy	222	NFNKATLKPEGQQAALDQLYTQLSNMDDPKDGSAAVVLGYTDRTGS	264
		: : : : : : : :	
Db	115	NFNKATLKPEGQQAALDQWYLSQLNDDPKDGSVVVLGFTDRTGS	157
		: : : : : : :	
RESULT	77		
Q6WA13		PRELIMINARY;	PRT; 157 AA.
ID	Q6WA13		
AC	Q6WA13;		
DT	05-JUL-2004	(TrEMBLrel. 27, Created)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	Outer membrane protein II (Fragment).		
GN	Name=ompA;		
OS	Citrobacter freundii.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		
OC	Enterobacteriaceae; Citrobacter.		
OK	NCBI_TaxID=546;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=MISC141;		
RX	MEDLINE=23001863; PubMed=14640415;		
RA	Wertz J.E., Goldstone C., Gordon D.M., Riley M.A.;		
RT	"A molecular phylogeny of enteric bacteria and implications for a		
RT	bacterial species concept.";		
RL	J. Evol. Biol. 16:1236-1248(2003).		
CC	-I- SIMILARITY: Belongs to the ompA family.		
DR	EMBL; AY301170; AAQ96064.1; -.		
DR	GO; GO:0016021; C: Integral to membrane; IEA.		
DR	GO; GO:009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.		
DR	GO; GO:0005198; F: structural molecule activity; IEA.		
DR	InterPro; IPR006664; Bac OmpA.		
DR	InterPro; IPR002368; OmpA.		
DR	InterPro; IPR006665; OmpA/MotB.		
DR	InterPro; IPR000498; OmpA_tmcm.		
DR	Pfam; PF00691; OmpA; 1.		
DR	Pfam; PF01389; OmpA membrane; 1.		
DR	PRINTS; PR01021; OMPADOMAIN.		
DR	PRINTS; PR01022; OUTRMMBAREA.		
DR	ProDom; PD000930; OmpA/MotB; 1.		
FT	NON_TER 1		
FT	NON_TER 157		
FT	NON_TER 157		
SQ	SEQUENCE 157 AA; 17004 MW; A3A61755346B741A CRC64;		
	Query Match	37.0%;	Score 674.5; DB 2; Length 157;
	Best Local Similarity	80.4%;	Pred. No. 4.7e-44;
	Matches 13;	Conservative 13;	Mismatches 12; Indels 7; Gaps 3;
Qy	103	DDLDIYTRLGGVWVRADSKGNYSTGVSRSEHDTGVSFVAGGVAVTRDIATRLLEYQW	162
		: : : : : : :	
Db	1	DDLDDYTRLGGVWVRADAKNNEG----	KDHDITGVSFVAGGVAVTPTATRLLEYQW 55
Qy	163	VNNIGDAGTVGTRPDNGMLSLGVSYRFG-QEDAAPVVPAPAPAPAPVATKHFTLKSDVLF	221
		: : : : : : :	
Db	56	TNNIGDANTVGGRPDNGLLSGVSYRFGQEEAAPVVV-APAPAPEVQTKHFTLKSDVLF	114
Qy	222	NFNKATLKPEGQQAALDQLYTQLSNMDDPKDGSAAVVLGYTDRTGS	264
		: : : : : : :	
Db	115	NFNKATLKPEGQQAALDQWYLSQLNDDPKDGSVVVLGFTDRTGS	157
		: : : : : : :	
RESULT	78		
Q6WA14		PRELIMINARY;	PRT; 157 AA.
ID	Q6WA14		
AC	Q6WA14;		
DT	05-JUL-2004	(TrEMBLrel. 27, Created)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	Outer membrane protein II (Fragment).		
GN	Name=ompA;		
OS	Citrobacter freundii.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		
OC	Enterobacteriaceae; Citrobacter.		


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CC -!- SIMILARITY: Belongs to the ompA family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L08448; AAA24959.1; -.
DR HSP; P02934; 1BXW.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR006690; OmpA LIKE.
DR InterPro; IPR000498; OmpA_cm.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRODOM; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OMPA; FALSE NEG.
KW Direct protein sequencing; Fimbria; Outer membrane; Porin; Signal;
KW Transmembrane.
FT SIGNAL 1 21
FT CHAIN 22 359 Outer membrane protein P5.
FT DISULFID 332 344 By similarity.
FT DOMAIN 278 322 OmpA-like.
FT SEQUENCE 359 AA; 38340 MW; 576B1C59B4818C37 CRC64;
Query Match 36.4%; Score 662.5; DB 1; Length 359;
Best Local Similarity 43.3%; Pred. No. 1.2e-42;
Matches 155; Conservative 49; Mismatches 121; Indels 33; Gaps 9;
QY 1 MKAFVLNAAKPDNTWYAGKGLGWSQYHD----TCFYNGNGQNNNGPTRNDQLGAGAFGG 56
D 13 LAASVAQAQAPQENTFYAGVAGKAGQSPHGDINNNGAIIKGLSSNGYRRNTFTYGVFGG 72
QY 57 YQV-----NPYLGFEMGYDNLGRMAYKGVSDNGAFKAQ---GVOLTKAGLPIPTDLDIY 108
D 73 YQILNQDNFGLAAELGYDDFGRAKL---EAGKPKAKHTNHGAYLSLKGSEYVLDGLDVY 129
QY 109 TRLGGMWRADSKGNVASTGV---SRSEHDTGVSVPFAGGVAVVTRDIATRLLEYQWNN 165
D 130 GKAGVALVRSYKFFEDANGTRDHKKRHTARASGLFAGVAGAYAVLPDLAVRLEYQMLTR 189
QY 166 IG-----DAGTVCTRPDNGMLSLGVSRYRFGQEDAAPVAPAPAPAPAEVATKHTLXSD 218
D 190 VGKYPQDKPNTAINYNPWIGCINAGISYRFGQGE-APVVA-----APEVMYKTFSLNSD 243
QY 219 VLEFNKATLKPEGOALDQLYTQLSNMDPKDGSVAVLGYTDRIGSAYNQOLSEKRAQS 278
D 244 VTFAPGKANLKPOAQTLDVSYGEISQV---KSRKVAVAGYINRIGSDAFNVKLSQERADS 301
QY 279 VVDYLVAKGIPAGKISARGMESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGK 336
D 302 VANYFVAKGVAADSAISATGYGEANPVTGATCDQVKGKRALIACIAPDRRVEIANGTK 359
RESULT 83
O86254 PRELIMINARY; PRT; 360 AA.
ID O86254
AC O86254;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Outer membrane protein (Fragment).
GN Name=omp;
OS Haemophilus sp.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=740;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=16N;
RX MEDLINE=99081716; PubMed=9864189;
RA Goussset N., Rosenau A., Sizaret P.Y., Quentin R.;
RT "Nucleotide sequences of genes coding for fimbrial proteins in a
RT cryptic genospecies of Haemophilus spp. isolated from neonatal and
RT genital tract infections.";
RL Infect. Immun. 67:8-15(1999).
CC -!- SIMILARITY: Belongs to the ompA family.
CC EMBL; AJ007317; CAA07454.1; -.
CC HSP; P02934; 1BXW.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
CC GO; GO:0005198; F:structural molecule activity; IEA.
CC InterPro; IPR006664; Bac_OmpA.
CC InterPro; IPR002368; OmpA.
CC InterPro; IPR006665; OmpA/MotB.
CC InterPro; IPR006690; OmpA LIKE.
CC Pfam; PF00691; OmpA; 1.
CC Pfam; PF01389; OmpA_membrane; 1.
CC PRINTS; PR01021; OMPADOMAIN.
CC PRODOM; PD000930; OmpA/MotB; 1.
CC PROSITE; PS01068; OMPA; 1.
FT NON TER 360 360
FT SEQUENCE 360 AA; 38415 MW; A320915051CDD69 CRC64;
Query Match 36.3%; Score 662; DB 2; Length 360;
Best Local Similarity 44.6%; Pred. No. 1.3e-42;
Matches 160; Conservative 49; Mismatches 116; Indels 34; Gaps 12;
QY 1 MKAFVLNAAKPDNTWYAGKGLGWSQYHDTGYGNGF-----QNNNGPTRNDQLGAGAF 54
D 13 LAASIAQAQAPQENTFYAGVAGKAGQASPHD-GISKNSFIADILGLDNYGYNEN-SFTYGVF 70
QY 55 GGYQV---NPYLGFEMGYDNLGRMAYK-GVSDNGAFK--AQGVOLTKAGLGYPTDLDI 107
D 71 GGYQILNRDLNLGLAVELGYDDFGRVKFKPSFGKTSIKHTNHGAHLSFKGSEYVNLGLDV 130
QY 108 YTRLGGMWRADSKGNVASTGV---SRSEHDTGVSVPFAGGVAVVTRDIATRLLEYQWNN 164
D 131 YGKAGVALVRSYK-FTDANGARKRANSHLSRTGLFAGVAGAYAVLPDLAVRLEYQMLT 189
QY 165 NIGDAGT-----VGTTRPDNGMLSLGVSRYRFGQEDAAPVAPAPAPAEVATKHTLKS 217
D 190 RVGKLRQTQETHNSSVDYNPWIGSINAGVSRYFGQ-GAAPVA-----APEVSKTFNLNS 243
QY 218 DVLFPNFKATLKPEGOALDQLYTQLSNMDPKDGSVAVLGYTDRIGSAYNQOLSEKRAQ 277
D 244 DVNFAFGKANLKPOAALDGIYGEIAQVN--SAKVAVAGYTDRIGSDFNVKLSQRAE 301
QY 278 SVVDYLVAKGIPAGKISARGMESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGK 336
D 302 TVANYFVAKGVSADSAISATGYGKANPVTGATCDQVKGKRALIACIAPDRRVEIANGTK 360
RESULT 84
O6XAY6 PRELIMINARY; PRT; 378 AA.
ID O6XAY6
AC O6XAY6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat-modifiable outer membrane protein.
GN Name=ompA;
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=PH540;

```


DR	GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR	GO; GO:0005198; F:structural molecule activity; IEA.
DR	InterPro; IPR006664; Bac OmpA.
DR	InterPro; IPR002368; OmpA.
DR	InterPro; IPR006665; OmpA/MotB.
DR	InterPro; IFR000498; OmpA_tmcm.
DR	Pfam; PF00691; OmpA; 1.
DR	Pfam; PF01389; OmpA membrane; 1.
DR	PRINTS; PR01021; OMPADOMAIN.
DR	PRINTS; PR01022; OUTRMMORNAE.
DR	ProDom; PD000930; OmpA/MotB; 1.
SQ	SEQUENCE 367 AA; 39234 MW; 08D2318189CC4291 CRC64;
	Query Match 36.1%; Score 658.5; DB 2; Length 367;
	Best Local Similarity 41.9%; Pred. No. 2.4e-42;
	Matches 155; Conservative 61; Mismatches 107; Indels 47; Gaps 13;
Qy	1 MKAIFFVUNAAPKONTWTYAGKLHWSQYHD--TGF---YGNGFQNNNGPTRNDQLGAGAFG 55
Dd	11 LSAAVAQAAPQANTFYAGAKAGWASPHDGLTQPDHKDGGEF-----GINRN-SVTYGVF 65
Qy	56 GYQV----NPLYCFEMGYDWLGRM----AYKG-SVDNGAFK--AQGVQLTAKLGYPITDD 104
Dd	66 GYQLLNQNNGFLATELGYDYDFVRVGKNKTPEGENSDKRAAKHSAGHAHLSLKPSYEVPVN 125
Qy	105 LDIIYTRLCGMVMWRADSKNGNYASTCVSRSE----HDTGVSPVFAGGVWEAVTRDIATRL 160
Dd	126 LDVVYKGVVALVRND---YYVQQNVAKDSRIKAHLKPSSLGLLAGLEVAITPELAARVEY 182
Qy	161 QWNNIIGD-----AGTVGTR-----PDNGMLSLGSYSYRFPGDEDAAPVVAAPAPAPEV 208
Dd	183 QYLNRVGNLDKAARKTANIEGTNFQYSPDIHSSVAGLSYRFGQ-----GAAPVEAPEV 235
Qy	209 ATKHEFTLSKVLENFNKATIKPBEGQALDQLYTOLSNMDPKGSAVLGYTDRTIGSEAYN 268
Dd	236 VTKNFAEPSDVLPDFGKSLSKPAATAISLDAAHAEISNLGLANPAIQVNGYTDRIGKEASN 295
Qy	269 QQLSEKRAQSVDVYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRV 328
Dd	296 LKLSQRRAETIVANYIVSKTNPNANTVAVGEANPVTGHICDCAVKGRKALLIACLAPDRV 355
Qy	329 EIEVKGYKEV 338
Dd	356 EIQVQSGKEV 365
RESULT	90
QYRQ28	PRELIMINARY; PRT; 378 AA.
ID	AC Q9RQ28;
DC	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	23-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE	Outer membrane protein PomA (Heat-modifiable outer membrane protein).
DN	Name=pomA; Synonyms=ompA;
OS	Pasteurella haemolytica.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC	Pasteurellaceae; Mannheimia.
OX	NCBI_TaxId=75985;
RX	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=89010807N;
RX	MEDLINE=99386907; PubMed=10456961;
RA	Zeng H., Pandher K., Murphy G.L.;
RT	"Molecular cloning of the Pasteurella haemolytica pomA gene and identification of bovine antibodies against PomA surface domains.";
RL	Infect. Immun. 67:4968-4973(1999).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=PH2, and PH202;
RX	PubMed=15317779; DOI=10.1128/JB.186.17.5741-5752.2004;
RA	Davies R.L., Lee I.;

"Sequence diversity and molecular evolution of the heat-modifiable outer membrane protein gene (ompA) of Mannheimia (Pasteurella) haemolytica, Mannheimia glucosida, and Pasteurella trehalosii." J. Bacteriol. 186:5741-5752(2004).

-/- SIMILARITY: Belongs to the ompA family.

DR EMBL; AF133259; AAD53408.1; -

DR EMBL; AY244653; AAO85781.1; -

DR EMBL; AY244655; AAO85783.1; -

DR HSSP; P02934; 1BXW.

DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.

DR GO; GO:0005198; F: structural molecule activity; IEA.

DR InterPro; IPR006664; Bac_OmpA.

DR InterPro; IPR002368; OmpA.

DR InterPro; IPR006665; OmpA/MotB.

DR InterPro; IPR00498; OmpA_tmam.

DR Pfam; PF00691; OmpA; 1.

DR Pfam; PF01389; OmpA membrane; 1.

DR PRINTS; PR01021; OMFADOMAIN.

DR PRINTS; PR01022; OUTRMMORANE.

DR ProDom; PD000930; OmpA/MotB; 1.

SQ SEQUENCE 378 AA; 40460 MW; 60D8E36AAD32P2EA CRC64;

Query Match 36.1%; Score 657; DB 2; Length 378;
Best Local Similarity 41.1%; Pred. No. 3.3e-42;
Matches 155; Conservative 60; Mismatches 112; Indels 50; Gaps 12;

Qy 1 MKAIFVLNAAPKONTWYAGKLGWSQYHD-----TGFYNGGFO--NNNGPTRNDOLGA 51
Db 11 LSAAVAQAQAQANTFYAGAKAGWASFDGLTQPDNTDYDGGINLGINLEN-SVTV 69

Qy 52 GAFGGYQV---NPYLGFEMGYDMLGRM-----AYKG-SVDNGAFK--AQGVLTAKLGY 100
Db 70 GVFGYQILNQNNFGLATELGYDFGRVGRNGTTFSGDDKDKTAAKHSAHGAHLSLKPSYE 129

Qy 101 ITDDLDIYTRLGGMWRADSKNTASTGVSSE-----HDTGVSPVFAGGVEWATRDIA 156
Db 130 VVPNLVDYGVKGVVALVRND---YVQVQHVQKDSRIKVNHLKPSLLGLAGLEYAITPELAA 186

Qy 157 RLEYQWNNIGDAG-----TVG-----TRPDNGLSLGVSYRFGQDAAPVWAPA 201
Db 187 RVEVQYLNVRGNLKDVAETTVGYLIPRGNTFYSPDIHSVAGLSYRFGQ-----GAA 239

Qy 202 PAPAPEVATKFTLKSVDLNFNFKATLKPEGQQALDQLYTQLSNMDPKDGSVAVVLGYTDR 261
Db 240 PVEAPEVTVTKNFAFSSDVLDFGKSLKPAATAASLDAHAHISNLGLANLAIQVNGYTD 299

Qy 262 IGSEAYNQOLSEKRAQSVVDLVAKGIPAGKISARGMESNPVTGNTCDNVKARAALIDC 321
Db 300 IGKEASNLKLSQRAETVANTIVSKGTNPANVTAVGYGEANPVTGHTCDVAKGRKALITAC 359

Qy 322 LAPDRRVIEVKGKVEV 338
Db 360 LAPDRRVIEVQGGKEV 376

RESULT 91
Q65T85 PRELIMINARY; PRT; 368 AA.

AC Q65T85;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE OmpA protein.
GN Name=ompA; ORFNames=MS1218;
OS Mannheimia succiniciproducens MBEL55E.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MBEL55E;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,

RA Kim C.H., Jeong H., Hur C.-G., Kim J.G.;
RT "the genome sequence of the capnophilic rumen bacterium Mannheimia succiniciproducens." Nat. Biotechnol. 0:0-0(2004).
RL EMBL; AE016827; AAU37825.1; -.
SQ SEQUENCE 368 AA; 38974 MW; 1AFB979D5D594B62 CRC64;

Query Match 35.9%; Score 655; DB 2; Length 368;
Best Local Similarity 42.7%; Pred. No. 4.5e-42;
Matches 154; Conservative 57; Mismatches 110; Indels 40; Gaps 13;

Qy 1 MKAIFVLNAAPKONTWYAGKLGWSQYHD-----TGFYNGGFO--NNNGPTRNDOLGA 59
Db 23 LAATAAQAAPQENTFYAGAKAGWASFDH-GY--TQYAEQVGSHTKSVTVYGVGGYQIF 79

Qy 60 ---NPYLGFEMGYDMLGRMAYKGSVDNGAFKAQ---GVQLTAKLGY-----PITDLD 106
Db 80 NRDNGLGLAVELGYDDFCRAALR---TNGATSAKHTNHGAHLSLKPSYDLGALAPVLSGLD 136

Qy 107 IYTRLGGMWRADSKGNYA-STGVSR---EHTGVSPVFAGGVEWATR--DIATRLLEY 160
Db 137 VYGVKGAALVRSDYKVNDSYSGFNKSDFDADHSLSKTSLLLGAGLEYALPSLPELAFLLEY 196

Qy 161 QWNNNIGDAGTV-GTR-----PDNGLSLGVSYRFGQDAAPVWAPAAPAPAPAPAPAPAPAP 215
Db 197 QWLNKVKGLNANGTREDFYTPETHSVTAGVSYRFGQVAAPV-----AEVVSKTFTL 249

Qy 216 KSDVLFNFKATLKPEGQQALDQLYTQLSNMDPKDGSVAVVLGYTDRIGSEAYNQOLSEKR 275
Db 250 NSDVTFAFGKATLKPEASISLDNIYGEIAQV--QSPAVSVAGYADRIGKEAANKLSQRR 307

Qy 276 AQSVVDLVAKGIPAGKISARGMESNPVTGNTCDNVKARAALIDCLAPDRRVIEVKG 335
Db 308 AETVANYLVSKGVAQNAITATGYGEANPVTGNTCDVAKGRKALITACIAPDRRVSVSQGT 367

Qy 336 K 336
Db 368 K 368

RESULT 92
Q6XAX6 PRELIMINARY; PRT; 367 AA.

AC Q6XAX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat-modifiable outer membrane protein.
GN Name=ompA;
OS Mannheimia glucosida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=85401;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PH344;
RX PubMed=15317779; DOI=10.1128/JB.186.17.5741-5752.2004;
RA Davies R.L., Lee I.;
RT "Sequence diversity and molecular evolution of the heat-modifiable outer membrane protein gene (ompA) of Mannheimia (Pasteurella) haemolytica, Mannheimia glucosida, and Pasteurella trehalosii." J. Bacteriol. 186:5741-5752(2004).
CC -/- SIMILARITY: Belongs to the ompA family.
DR EMBL; AY244664; AAO85792.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR00498; OmpA_tmam.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.

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DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBRANE.
DR ProDom; PD000930; OmpA/MotB; 1.
SQ SEQUENCE 367 AA; 39136 MW; 07C39365A607958F CRC64;

Query Match 35.8%; Score 652.5; DB 2; Length 367;
Best Local Similarity 41.4%; Pred. No. 7e-42;
Matches 154; Conservative 61; Mismatches 106; Indels 51; Gaps 13;

QY 1 MKAIFVLNAAPKONTWYAGGKLGWSQYHD--TGF---YNGGFQNNNGPTRNDQLGAGAFG 55
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 11 LSAAAVAQAAPQANTFYAGAKAGWASPHDGLTQFDHKDGGEF---GINRN-SVTYGVFG 65
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 56 GYQV---NPVLGPEMGYDMLGRMAYKGSV-----DNGAFK--AQCGLTAKLGYPI 102
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 GYQILQNNFGLATELGYDYFGRV--RGNTTFAGDDKEKTAAKHSAHAHLSLPSYEV 123
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 103 DDLDIYTRLGMMWRADSKNGYASTGVSRSE---HDTGVSPVFAGGVEMAVTRDIATRL 158
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 PNLDDYGVKGVVALVRND---YVQQNVAKDSRIKAHNLKPSLLLGAGLEYAITPELAARV 180
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 159 EYQWVNNIGD-----AGTVGTR-----PONGMLSLGVSFRGQEDAAPVVAAPAPAP 206
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 EYQVLRVGNLDKAARKTANIEGTFQYSPDIHVSAGLSYRFGQ-----GAAPVEAP 233
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 207 EVATKFTLKSDDLFLNFENKATLKPEGOQALDQLYTQLSNMMPKDGSAVVLGYTDRIGSEA 266
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 234 EVVTKNFAFSSDVLDFDKSKSLKPAATSLDAAHAEISNLGLANLAIQVNGYTDRIKGEA 293
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 267 YNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDR 326
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 294 SNLKLSQRAETVANYIVSKGTNPANVTAVGGEANPVTGHTCDVAVGRKALIACLAPDR 353
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 327 RVEIEVKGYKEV 338
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 354 RVEIQVQGSKEV 365
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 93
Q6XAX8 PRELIMINARY; PRT; 367 AA.
AC Q6XAX8
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Heat-modifiable outer membrane protein.
GN Name=ompA;
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PH296;
RX PubMed=15317779; DOI=10.1128/JB.186.17.5741-5752.2004;
RA Davies R.L., Lee I.;
RT "Sequence diversity and molecular evolution of the heat-modifiable
RT outer membrane protein gene (ompA) of Mannheimia (Pasteurella)
RT haemolytica, Mannheimia glucosida, and Pasteurella trehalosi.";
RL J. Bacteriol. 186:5741-5752(2004).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; AY244662; AAO85790.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBRANE.
SQ SEQUENCE 367 AA; 39912 MW; 8FE6E7F979D37411 CRC64;

DR ProDom; PD000930; OmpA/MotB; 1.
SQ SEQUENCE 367 AA; 39152 MW; 07DE4F7867DB8853 CRC64;

Query Match 35.7%; Score 650.5; DB 2; Length 367;
Best Local Similarity 41.4%; Pred. No. 9.9e-42;
Matches 154; Conservative 61; Mismatches 106; Indels 51; Gaps 13;

QY 1 MKAIFVLNAAPKONTWYAGGKLGWSQYHD--TGF---YNGGFQNNNGPTRNDQLGAGAFG 55
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 11 LSAAAVAQAAPQANTFYAGAKAGWASPHDGLTQFDHKDGGEF---GINRN-SVTYGVFG 65
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 56 GYQV---NPVLGPEMGYDMLGRMAYKGSV-----DNGAFK--AQCGLTAKLGYPI 102
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 GYQILQNNFGLATELGYDYFGRV--RGNTTFAGDDKEKTAAKHSAHAHLSLPSYEV 123
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 103 DDLDIYTRLGMMWRADSKNGYASTGVSRSE---HDTGVSPVFAGGVEMAVTRDIATRL 158
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 PNLDDYGVKGVVALVRND---YVQQNVAKDSRIKAHNLKPSLLLGAGLEYAITPELAARV 180
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 159 EYQWVNNIGD-----AGTVGTR-----PONGMLSLGVSFRGQEDAAPVVAAPAPAP 206
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 EYQVLRVGNLDKAARKTANIEGTFQYSPDIHVSAGLSYRFGQ-----GAAPVEAP 233
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 207 EVATKFTLKSDDLFLNFENKATLKPEGOQALDQLYTQLSNMMPKDGSAVVLGYTDRIGSEA 266
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 234 EVVTKNFAFSSDVLDFDKSKSLKPAATSLDAAHAEISNLGLANLAIQVNGYTDRIKGEA 293
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 267 YNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDR 326
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 294 SNLKLSQRAETVANYIVSKGTNPANVTAVGGEANPVTGHTCDVAVGRKALIACLAPDR 353
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 327 RVEIEVKGYKEV 338
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 354 RVEIQVQGSKEV 365
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 94
Q6XAX9 PRELIMINARY; PRT; 373 AA.
AC Q6XAX9
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Heat-modifiable outer membrane protein.
GN Name=ompA;
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PH196;
RX PubMed=15317779; DOI=10.1128/JB.186.17.5741-5752.2004;
RA Davies R.L., Lee I.;
RT "Sequence diversity and molecular evolution of the heat-modifiable
RT outer membrane protein gene (ompA) of Mannheimia (Pasteurella)
RT haemolytica, Mannheimia glucosida, and Pasteurella trehalosi.";
RL J. Bacteriol. 186:5741-5752(2004).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; AY244661; AAO85789.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBRANE.
DR ProDom; PD000930; OmpA/MotB; 1.
SQ SEQUENCE 373 AA; 39912 MW; 8FE6E7F979D37411 CRC64;
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Query Match 35.7%; Score 650.5; DB 2; Length 373;
Best Local Similarity 40.9%; Pred. No. 1e-41;
Matches 153; Conservative 61; Mismatches 111; Indels 49; Gaps 12;

QY 1 MKAIFVLAAPKONTWYAGKLGWSQYHD--TGF-----YGNFQNNNGPTRNDQLGAGAF 54
DB 11 LSAAVAQAAPQANTFYAGAKAGWASPHDGLTQFDHKKDGGGFEFSIQYGINRN-SVYGVF 69
QY 55 GGYQV---NPVLGEMGVDMGRMAYKGSV-----DNGAFK--AQCQVLTAKLGVPI 101
DB 70 GGYQLLNQNNFGLATELGVDYFGRV--RGNTTFAGDDKEKTAAKSAHGAHLSLKPSYEV 127
QY 102 TDDLDIYTRLGGMWRADSKGNVASTGVSRBE---HDTGVSPVFAGGVEMAVTRDIATR 157
DB 128 VPNLDVYGVGVVALVRND---YVQQRVAKDSRIKAHNLKPSLLILGAGLEVAITPELAAR 184
QY 158 LEYQWVNNIGDAG-----TVGTR-----PDNGMLSLGVSYRFGQEDAAPVAPAPAP 204
DB 185 VEYQYLNVRVGNLDKAVRTVSLPTGTNFQYSPDIHSVSAGLSYRFGQ-----GAAPVE 237
QY 205 APEVATKFTLKSDVLFNFNFKATLKPEGOQALDQLYTQLSNMMDPKDGSVAVLYGTYDRIGS 264
DB 238 APEVVTKNFAPSSDVLFFPGSSLKPAATSLDAHAHISNLGLANLAIQVNGYTDRLGK 297
QY 265 EAYNQOLSEKRAQSVYDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKABAAALIDCLAP 324
DB 298 EASNLKLSORRAETVANYIVSKGTNPANVTAVGYGEANPVTGHTCDAVKGRKALIACLAP 357
QY 325 DRRVEIEVKYKEV 338
DB 358 DRRVEIQVQSKEV 371

RESULT 95
Q6WAF2 ID Q6WAF2 PRELIMINARY; PRT; 162 AA.
AC Q6WAF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Outer membrane protein II (Fragment).
GN Name=ompA;
OS Serratia plymuthica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=82996;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISC297;
RX MEDLINE=23001863; PubMed=14640415;
RA Wertz J.E., Goldstone C., Gordon D.M., Riley M.A.;
RT "A molecular phylogeny of enteric bacteria and implications for a bacterial species concept.";
RL J. Evol. Biol. 16:1236-1248(2003).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; AY3011201; AAQ36095.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR000498; OmpA_tmam.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBRANEA.
DR ProDom; PD000930; OmpA/MotB; 1.
FT NON_TER 1 162
FT SEQUENCE 162 AA; 17427 MW; F98576CEB5D29C30 CRC64;

Query Match 35.5%; Score 647.5; DB 2; Length 162;
Best Local Similarity 79.7%; Pred. No. 5.9e-42;
Matches 126; Conservative 13; Mismatches 18; Indels 1; Gaps 1;

QY 103 DDLDIYTRLGGMWRADSKGNVASTGVSRSEHDTGVSPVFAGGVEMAVTRDIATRLLEYOW 162
DB 1 DDLDIYTRLGGMWRADSKGNVASTGVSRSEHDTGVSPVFAGGVEMAVTRDIATRLLEYOW 59
QY 163 VNNIGDAGTGTTRPDNGMLSLGVSYRFGQEDAAPVAPAPAPAPAPAPAPVETATKHTLKSDDLFLN 222
DB 60 VSNIGDAGTGTTRPDNGMLSLGVSYRFGQEDAAPVAPAPAPAPAPAPVETATKHTLKSDDLFLN 119
QY 223 FNKATLKPEGOQALDQLYTQLSNMMDPKDGSVAVLYGTYD 260
DB 120 FNKATLKPEGOQALDQLYTQLSNMMDPKDGSVAVLYGTYD 157

RESULT 96
Q6WAF4 ID Q6WAF4 PRELIMINARY; PRT; 162 AA.
AC Q6WAF4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Outer membrane protein II (Fragment).
GN Name=ompA;
OS Serratia plymuthica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=82996;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISC145;
RX MEDLINE=23001863; PubMed=14640415;
RA Wertz J.E., Goldstone C., Gordon D.M., Riley M.A.;
RT "A molecular phylogeny of enteric bacteria and implications for a bacterial species concept.";
RL J. Evol. Biol. 16:1236-1248(2003).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL; AY3011199; AAQ96093.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_tmam.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBRANEA.
DR ProDom; PD000930; OmpA/MotB; 1.
FT NON_TER 1 162
FT SEQUENCE 162 AA; 17427 MW; F98576CEB5D29C30 CRC64;

Query Match 35.5%; Score 647.5; DB 2; Length 162;
Best Local Similarity 79.7%; Pred. No. 5.9e-42;
Matches 126; Conservative 13; Mismatches 18; Indels 1; Gaps 1;

QY 103 DDLDIYTRLGGMWRADSKGNVASTGVSRSEHDTGVSPVFAGGVEMAVTRDIATRLLEYOW 162
DB 1 DDLDIYTRLGGMWRADSKGNVASTGVSRSEHDTGVSPVFAGGVEMAVTRDIATRLLEYOW 59
QY 163 VNNIGDAGTGTTRPDNGMLSLGVSYRFGQEDAAPVAPAPAPAPAPAPVETATKHTLKSDDLFLN 222
DB 60 VSNIGDAGTGTTRPDNGMLSLGVSYRFGQEDAAPVAPAPAPAPAPVETATKHTLKSDDLFLN 119
QY 223 FNKATLKPEGOQALDQLYTQLSNMMDPKDGSVAVLYGTYD 260
DB 120 FNKATLKPEGOQALDQLYTQLSNMMDPKDGSVAVLYGTYD 157


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Db 124 PHLDTYGVKGVVALVRND---YVQONVAKDSRIKAHNKLPKSLILGAGLEYAITPELAARV 180
QY 159 EYQWYNNIGD-----AGTVGTR-----PQNGMLSLGVSYRFGQEDAAPVVAPAPAP 206
Db 181 EYQVLRVGNLDKAARKTANIEGTFNQYSPDIHSVAGLSYRFGQ-----GAAPVEAP 233
QY 207 EVATKHTLKSDVLFNFKATILKPGQOALDOLYTLQLSNMDPKDGSAAVVLGYTDRIGSEA 266
Db 234 EYVTKNFAFSDVLPDFGKSLKPAATSLDAAHAEISNLGLANLAIQVNGYTDRIKSEA 293
QY 267 YNOQLSEKRAQSVVDVLVAKGIPACKIGARGMGESNPVTGNTCDNVKARAALIDCLAPDR 326
Db 284 SNLKSQRAAEVANYIVSKGTPNPANVTAVGGEANPVGTGTCDAVKGKALIACLAPDR 353
QY 327 RVEIEVKGYKEV 338
Db 354 RVEIQVQSGKEV 365

RESULT 99
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AC Q6WAF3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Outer membrane protein II (Fragment).
GN Name=OmpA;
OS Serratia plymuthica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=82996;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISC8;
RA MEDLINE=23001863; PubMed=14640415;
RT "A molecular phylogeny of enteric bacteria and implications for a bacterial species concept.";
RL J. Evol. Biol. 16:1236-1248(2003).
CC -I- SIMILARITY: Belongs to the ompA family.
DR EMBL; AY301200; AAQ96094.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_tmemb.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01389; OmpA membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMBRANE.
DR PRODOM; PD000930; OmpA/MotB; 1.
FT NON_TER 162 162
FT SEQUENCE 162 AA; 17455 MW; 963226ECF65C60C CRC64;

Query Match 35.4%; Score 644.5; DB 2; Length 162;
Best Local Similarity 79.7%; Pred. No. 1e-41;
Matches 126; Conservative 13; Mismatches 18; Indels 1; Gaps 1;

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Db 1 DDLDTYRLGGMWRADSKGNVYGN-GRLSHDHDTGSPVLAAGVEYALTKWATRLDYQF 59
QY 163 VNNIGDAGTVTRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAEVATKHTLKSDVLFN 222
Db 60 VSNIGDAGTVGARPNTMLSLGVSYRFGQDDVAVPAPAPAPVETKRTKTLKSDVLFN 119
QY 223 FNKATLKPGQOALDOLYTLQLSNMDPKDGSAAVVLGYTD 260
Db 120 FNKATLKPGQOALDOLYTLQLSNMDPKDGSAAVVLGYTD 157

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RESULT 100
Q6PSK4 PRELIMINARY; PRT; 360 AA.
AC Q6PSK4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Outer membrane protein II (Fragment).
GN Name=OmpA';
OS Pasteurella trehalosi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=47735;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PH246; PH252, PH254, and PH68;
RX PubMed=15317779; DOI=10.1128/JB.186.17.5741-5752.2004;
RA Davies R.L., Lee I.;
RT "Sequence diversity and molecular evolution of the heat-modifiable outer membrane protein gene (ompA) of Mannheimia (Pasteurella) haemolytica, Mannheimia glucosida, and Pasteurella trehalosi.";
RL J. Bacteriol. 186:5741-5752(2004).
CC -I- SIMILARITY: Belongs to the ompA family.
DR EMBL; AY582756; AAS91722.1; -.
DR EMBL; AY582757; AAS91726.1; -.
DR EMBL; AY582758; AAS91730.1; -.
DR EMBL; AY582759; AAS91731.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_tmemb.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMBRANE.
DR PRODOM; PD000930; OmpA/MotB; 1.
SQ SEQUENCE 360 AA; 37979 MW; B24A3C6659A0D87A CRC64;

Query Match 34.6%; Score 630.5; DB 2; Length 360;
Best Local Similarity 40.2%; Pred. No. 3.3e-40;
Matches 145; Conservative 48; Mismatches 127; Indels 41; Gaps 7;

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Db 14 AVASANAAPANSVYVGAAGKAGWASFDHGISQIDHKGKGYG---INKNSVT-----YGA 64
QY 54 FGGYQVNPYLGFMGYDMLGRMAYKGSVDNGAPK-----AQGVQLTAKLGYPIITDLDI 107
Db 65 FVGYYIIDNLAAEVGYBYFGRVGRGLEOTKAGGSKKTRHSAHGTTIALKGYEIVISGLDT 124
QY 108 YTRLGGMWRADSKGNVASTGVSRSHEDTGSPVFAGGVWAVTRDIATRLLEYQWVNNIG 167
Db 125 YAKAGIALVNNYSYKTVNVDIKVPTKTSRFQSSLLILGAGVEYAITPSLGARLEYQWLNAG 184
QY 168 DA-----GTVGT--RPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAEVATKHTLTKS 217
Db 185 KASVATLRRMGVEGSDYRDPDISSVAGLTVRFQG-----GAAPVAPEIETVTKNFAFSS 237
QY 218 DVLLENFKATLKPGQOALDOLYTLQLSNMDPKDGSAAVVLGYTDRIGSEAYNQQLSEKRAQ 277
Db 238 DVLDFGKALNLSAAKSLDAAHAEIQNLGATPAIQNGYTDRIKGPAPWALSQRKAE 297
QY 278 SVVDYLVAKGIPACKIGARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKE 337
Db 298 SVANYWYKGVAPESITAVGVGRANPVGTGNTCDAVKGRKALIACLAPDRRVELVQVQSGKE 357
SQ SEQUENCE 360 AA; 37979 MW; B24A3C6659A0D87A CRC64;

Query Match 34.6%; Score 630.5; DB 2; Length 360;
Best Local Similarity 40.2%; Pred. No. 3.3e-40;
Matches 145; Conservative 48; Mismatches 127; Indels 41; Gaps 7;

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Db 358 V 358

Search completed: September 20, 2005, 21:38:34
Job time : 184 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 20, 2005, 21:29:43 ; Search time 42 Seconds
(without alignments)
611.411 Million cell updates/sec

Title: US-09-647-309A-2

Perfect score: 1822

Sequence: 1 MKAIFVLNAAAPKONTWYAGG.....DRRVEIEVKGKVEVTPQQA 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Issued_Patents_AA.*

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5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1781	97.7	385	4	US-09-489-039A-7451
2	1771	97.2	335	3	US-08-836-500A-2
3	1771	97.2	335	4	US-09-679-750-2
4	1279	70.2	384	4	US-09-543-681A-7922
5	984	54.0	179	3	US-08-836-500A-4
6	984	54.0	179	4	US-09-679-750-4
7	671	36.8	364	4	US-09-809-665A-151
8	667	36.6	364	4	US-09-418-980-8
9	662.5	36.4	359	1	US-08-457-997B-2
10	662.5	36.4	359	3	US-08-467-722A-2
11	662.5	36.4	359	4	US-09-451-184-2
12	646.5	35.5	369	4	US-09-809-665A-153
13	639.5	35.1	369	4	US-09-418-980-10
14	586.5	32.2	338	1	US-08-210-394-1
15	379	20.8	72	3	US-08-836-500A-6
16	379	20.8	72	4	US-09-679-750-6
17	281	15.4	53	3	US-08-836-500A-8
18	281	15.4	53	4	US-09-679-750-8
19	242.5	13.3	379	4	US-09-328-352-5219
20	231.5	12.7	351	4	US-09-252-991A-30094
21	226	12.4	349	4	US-09-573-630A-2
22	199	10.9	235	4	US-09-252-991A-19595
23	193.5	10.6	259	4	US-09-328-352-5775
24	191	10.5	342	4	US-09-902-540-15847
25	184.5	10.1	566	4	US-09-489-039A-14179
26	182	10.0	220	4	US-09-489-039A-11012
27	182	10.0	226	2	US-08-572-447C-15

28	182	10.0	226	3	US-09-267-747-15	Sequence 15, Appl
29	181	9.9	161	2	US-08-572-447C-11	Sequence 11, Appl
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31	176.5	9.7	266	4	US-09-252-991A-18046	Sequence 18046, A
32	175	9.6	633	4	US-09-489-039A-13729	Sequence 13729, A
33	173.5	9.5	272	4	US-09-252-991A-29681	Sequence 29681, A
34	171	9.4	753	4	US-09-252-991A-17612	Sequence 17612, A
35	170	9.3	472	4	US-09-328-352-6870	Sequence 6870, Ap
36	168.5	9.2	214	2	US-08-572-447C-13	Sequence 13, Appl
37	168.5	9.2	214	3	US-09-267-747-13	Sequence 13, Appl
38	167.5	9.2	344	4	US-09-902-540-12463	Sequence 12463, A
39	167	9.2	409	4	US-09-902-540-12745	Sequence 12745, A
40	166.5	9.1	417	4	US-09-252-991A-26245	Sequence 26245, A
41	163.5	9.0	169	4	US-09-252-991A-19373	Sequence 19373, A
42	161	8.8	278	4	US-09-328-352-5824	Sequence 5824, Ap
43	158	8.7	257	4	US-09-328-352-6621	Sequence 6621, Ap
44	155	8.5	233	4	US-09-902-540-14590	Sequence 14590, A
45	151	8.3	374	4	US-09-902-540-13148	Sequence 13148, A
46	149	8.2	231	4	US-09-540-236-3827	Sequence 3827, Ap
47	146.5	8.0	172	4	US-09-674-779B-6	Sequence 6, Appl
48	143.5	7.9	172	4	US-09-674-779B-8	Sequence 8, Appl
49	143.5	7.8	152	4	US-09-540-236-3190	Sequence 3190, Ap
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51	137	7.5	314	4	US-09-252-991A-19600	Sequence 19600, A
52	136.5	7.5	172	4	US-09-674-779B-2	Sequence 2, Appl
53	136.5	7.5	552	4	US-09-540-236-2610	Sequence 2610, Ap
54	135	7.4	187	4	US-09-252-991A-29582	Sequence 29582, A
55	134	7.4	336	4	US-09-902-540-12749	Sequence 12749, A
56	133.5	7.3	543	4	US-09-902-540-13075	Sequence 13075, A
57	133	7.3	171	4	US-09-902-540-11370	Sequence 11370, A
58	132	7.2	166	4	US-09-489-039A-11724	Sequence 11724, A
59	131.5	7.2	196	4	US-09-328-352-6310	Sequence 6310, Ap
60	128.5	7.1	323	4	US-09-902-540-15219	Sequence 15219, A
61	128.5	7.1	544	4	US-09-902-540-15796	Sequence 15796, A
62	124.5	6.8	597	4	US-09-902-540-16615	Sequence 16615, A
63	124	6.8	113	4	US-09-902-540-16076	Sequence 16076, A
64	121.5	6.7	133	4	US-09-540-236-3221	Sequence 3221, Ap
65	120	6.6	153	6	5173294-2	Patent No. 5173294
66	120	6.6	153	6	5173294-2	Patent No. 5173294
67	116.5	6.4	268	4	US-09-902-540-16264	Sequence 16264, A
68	112	6.1	193	4	US-09-902-540-14516	Sequence 14516, A
69	105.5	5.8	1124	4	US-09-252-991A-26810	Sequence 26810, A
70	105	5.8	453	4	US-09-252-991A-20645	Sequence 20645, A
71	104	5.7	743	4	US-09-328-352-5073	Sequence 5073, Ap
72	104	5.7	1255	4	US-09-902-540-12628	Sequence 12628, A
73	101	5.5	180	4	US-09-543-681A-5543	Sequence 5543, Ap
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76	100	5.5	300	4	US-09-252-991A-27792	Sequence 27792, A
77	100	5.5	367	3	US-09-041-889-30	Sequence 30, Appl
78	100	5.5	367	4	US-09-417-264-30	Sequence 30, Appl
79	99.5	5.5	684	4	US-09-543-681A-4908	Sequence 4908, Ap
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81	97	5.3	192	4	US-09-198-452A-830	Sequence 830, App
82	97	5.3	218	4	US-09-438-185A-783	Sequence 783, App
83	96	5.3	117	4	US-09-252-991A-17204	Sequence 17204, A
84	95	5.2	273	4	US-09-328-352-6316	Sequence 6316, Ap
85	95	5.2	431	4	US-09-252-991A-33119	Sequence 33119, A
86	95	5.2	703	5	PCT-US95-06994-9	Sequence 9, Appl
87	94	5.2	182	4	US-09-489-039A-13005	Sequence 13005, A
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ALIGNMENTS

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RESULT 1
US-09-489-039A-7451
; Sequence 7451, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
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; SEQ ID NO 7451
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7451

Query Match          97.7%; Score 1781; DB 4; Length 385;
Best Local Similarity 99.1%; Pred. No. 1.2e-168;
Matches 336; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 2

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US-08-836-500A-2
; Sequence 2, Application US/08836500A
; Patent No. 6197929
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; APPLICANT: Baussant, Thierry
; APPLICANT: Haeuw, Jean-Francois
; APPLICANT: Nguyen Ngoc, Thien
; TITLE OF INVENTION: Carrier Protein Having an Adjuvant
; TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for
; TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines
; Patent No. 6197929
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,500A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Katz, Martin L.
; REGISTRATION NUMBER: 25,011
; REFERENCE/DOCKET NUMBER: PIE1514P0180US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
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Qy 243 LSNMPPKDGSAVLGYTDRISEAYNQOLSKRAQSVVDVYLVAKGIIPAGKISARGMGESN 302
Db 283 LANIDPTQGRVVVGYTDRIQSQYNNPLSEKRAQSVVDVYLVSKGIIPANSISABRGKEN 342
Qy 303 PVTGNTCDNVARAALIDCLAPDRRVEIEVKYKEVVTQP 342
Db 343 PVTGNTCDNVARAALIDCLAPDRRVEIEIQTTEVVVQP 382

RESULT 5
US-08-836-500A-4
; Sequence 4, Application US/08836500A
; Patent No. 6197929
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; APPLICANT: Bausant, Thierry
; APPLICANT: Haeuw, Jean-Francois
; APPLICANT: Nguyen Ngoc, Thien
; TITLE OF INVENTION: Carrier Protein Having an Adjuvant
; TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for
; TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines
; Patent No. 6197929
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockety, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,500A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Katz, Martin L.
; REGISTRATION NUMBER: 25,011
; REFERENCE/DOCKET NUMBER: PIE1514P0180US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5460
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-836-500A-4

Query Match 54.0%; Score 984; DB 3; Length 179;
Best Local Similarity 100.0%; Pred. No. 7.7e-90;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 APKONTWYAGKLGWSQYHDTGFGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEY 69
Db 1 APKONTWYAGKLGWSQYHDTGFGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEY 60

Qy 70 DWLGRMAYKGSYNNAGFAKAGIQITTKLSYPPVMDLDVYTRLCGMWRADSTATINATS 129
Db 61 DWLGRMAYKGSYNNAGFAKAGIQITTKLSYPPVMDLDVYTRLCGMWRADSTATINATS 120

Qy 130 SRSEHDTGSPVPFAGGVAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGVS 188
Db 121 SRSEHDTGSPVPFAGGVAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGVS 179

RESULT 6
US-09-679-750-4
; Sequence 4, Application US/09679750
; Patent No. 6780420
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; APPLICANT: Bausant, Thierry
; APPLICANT: Haeuw, Jean-Francois
; APPLICANT: Nguyen Ngoc, Thien
; TITLE OF INVENTION: Carrier Protein Having an Adjuvant
; TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for
; TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines
; Patent No. 6780420
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockety, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/679,750
; FILING DATE: 08-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,500
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Katz, Martin L.
; REGISTRATION NUMBER: 25,011
; REFERENCE/DOCKET NUMBER: PIE1514P0180US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-679-750-4

Query Match 54.0%; Score 984; DB 4; Length 179;
Best Local Similarity 100.0%; Pred. No. 7.7e-90;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 APKONTWYAGKLGWSQYHDTGFGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEY 69
Db 1 APKONTWYAGKLGWSQYHDTGFGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEY 60

Qy 70 DWLGRMAYKGSYNNAGFAKAGIQITTKLSYPPVMDLDVYTRLCGMWRADSTATINATS 129
Db 61 DWLGRMAYKGSYNNAGFAKAGIQITTKLSYPPVMDLDVYTRLCGMWRADSTATINATS 120

Qy 130 SRSEHDTGSPVPFAGGVAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGVS 188
Db 121 SRSEHDTGSPVPFAGGVAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGVS 179

Qy	1	MKAIFVLNAAPKONTWYAGGKLGWSQYHD-----TCFYCNGFQNNNGPTRNDQLCAGAFGG	56																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
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```
;
; ADDRESSSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
; 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Katz, Martin L.
; REGISTRATION NUMBER: 25,011
; REFERENCE/DOCKET NUMBER: PIE1514P0180US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-836-500A-8
;
; Query Match 15.4%; Score 281; DB 3; Length 53;
; Best Local Similarity 100.0%; Pred. No. 1.1e-20;
; Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 136 TGVSPVPAGGVWAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYR 188
; Db 1 TGVSPVPAGGVWAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYR 53
;
; RESULT 18
; US-09-679-750-8
; Sequence 8, Application US/09679750
; Patent No. 6780420
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; Baussant, Thierry
; Haeuw, Jean-Francois
; Nguyen Ngoc, Thien
;
; TITLE OF INVENTION: Carrier Protein Having an Adjuvant
; Effect, Immunogenic Complex Containing It, Process for
; Their Preparation, Nucleotide Sequence and Vaccines
;
; Patent No. 6780420
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
; 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/679,750
; FILING DATE: 08-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,500
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Katz, Martin L.
; REGISTRATION NUMBER: 25,011
; REFERENCE/DOCKET NUMBER: PIE1514P0180US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
;
; US-09-679-750-6
;
; Query Match 20.8%; Score 379; DB 4; Length 72;
; Best Local Similarity 100.0%; Pred. No. 3.2e-30;
; Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 117 RADSKGNVASTGVSRSEHDTGVSPFAGGVWAVTRDIATRLLEYQWVNNIGDAGTVGTRP 176
; Db 1 RADSKGNVASTGVSRSEHDTGVSPFAGGVWAVTRDIATRLLEYQWVNNIGDAGTVGTRP 60
;
; Qy 177 DNGMLSLGVSYR 188
; Db 61 DNGMLSLGVSYR 72
;
; RESULT 17
; US-08-836-500A-8
; Sequence 8, Application US/08836500A
; Patent No. 6197929
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; Baussant, Thierry
; APPLICANT: Haeuw, Jean-Francois
; APPLICANT: Nguyen Ngoc, Thien
;
; TITLE OF INVENTION: Carrier Protein Having an Adjuvant
; Effect, Immunogenic Complex Containing It, Process for
; Their Preparation, Nucleotide Sequence and Vaccines
;
; Patent No. 6197929
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
; 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

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; LENGTH: 53 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-679-750-8

Query Match      15.4%; Score 281; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 TCVSPVFAAGGVAVTRDIATRLLEYQWNNIGDAGTGTGTRPDNGMLSLGVSYSR 188
Db 1 TCVSPVFAAGGVAVTRDIATRLLEYQWNNIGDAGTGTGTRPDNGMLSLGVSYSR 53

RESULT 19
US-09-328-352-5219
; Sequence 5219, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328.352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5219
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5219

Query Match      13.3%; Score 242.5; DB 4; Length 379;
Best Local Similarity 26.1%; Pred. No. 1.5e-15;
Matches 91; Conservative 55; Mismatches 138; Indels 65; Gaps 12;

Qy 22 LGWSYHDTGFGYNGFON---NNGPTRNDQLGAGAFGGYQVNPYLGPFMGYDMLGRMAYK 78
Db 57 LGYT-FQDTQ-HNNGKGDELNGPELQDQLFVGAALGIELTPWLGFEEYNQV-----K 109

Qy 79 GSVNGAFKAQGVQLTAKLGYPITDDL-----DIYTRLGG-----MWRADS 120
Db 110 GDVDGLAAGAEBYKQKQINGNFVTSDLITKNYDSKIKPYLLGAGHYKYEIPDLSYHNDE 169

Qy 121 KGNVASTGVSRSRSHDTGVSVPFAGGVAVTRDIATRLLEYQWNNIGDAGTGTGTRPDNGM 180
Db 170 EGTLGAGV-----GAFWRLNDALSLRTEARGTYNFDKFWNYT-----AL 210

Qy 181 LSLGVSYSYRFGQEDAAPVAVAP-----APAEVATKHTLKSVDLNFNFKATLKPQGOQ 234
Db 211 AGLNVVLGGHLKPAAPVVEVAPVETTPVAPQPELTDLNMLRVFFDTNKSNIKQYKP 270

Qy 235 ALDQLYTLQSNMPPKDGSAVVLGYDTRIGSEAYNQQLSEKRAQSVVDYLVAK-GIPAGKI 293
Db 271 BIAKVAEKL--EYNATARIEGHTDNTGPKRLNERLSLARANSVKALVNEYNVDASRL 328

Qy 294 SARGHGENPVTGNTCDNVKARAALDCLAPDRRVEIEVKYKEVVTP 342
Db 329 STQGFAPWQDPIADNKTKEGRAM-----NRRVFATITGSRVTVVQP 368

RESULT 20
US-09-252-991A-30094
; Sequence 30094, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
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; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30094
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30094

Query Match      12.7%; Score 231.5; DB 4; Length 351;
Best Local Similarity 26.0%; Pred. No. 1.7e-14;
Matches 82; Conservative 43; Mismatches 87; Indels 103; Gaps 14;

Qy 97 LGYPITDDLDIYTRLGGVWRADSKGNVAS-----TGVSRSEH-----DTGVSVPVFA 143
Db 58 IGYFLTDDVELALSGBY---HVRGYETGNKKVHGNLTSLDAIYHFGTPGVGLRPPVS 114

Qy 144 GGV-----EWAVTRDIATRLLEYQWNNI-----GDAGTGTGTRPDNG-- 179
Db 115 AGLAHQNTWNSDSQGRQOMTWANIGAGLYYFTENFFAKASLDGQYGL--EKRDNGHQ 172

Qy 180 ---MLSLGVSYSYRFGQEDAAPVAVAPAPAPAEVAT----- 210
Db 173 GEWMAGLGVGFNFGGSKA----APAEFPVADVCSDSNDGVCNVDKCPDTPANVTVDAN 228

Qy 211 -----KHFTLKSDVLFENFKATILKPSGQALDQLYTLQLSNM-----DPKDGSAVVLGYT 259
Db 229 GCPAAVEVRVQLDVRFDKSKVK-----ENSYADIKNLADFMKQYFSTSTTVEGHT 281

Qy 260 DRIGSEAYNQQLSEKRAQSVVDYLVAK-GIPAGKISARGMGESNPVTGNTCDNVKARAAL 318
Db 282 DSVGTDAYNQKLSERRANAVRDVLVNEYGVGEGGRVNAVGYGESRPV----ADNATAEGRA 337

Qy 319 IDCLAPDRRVEIEVK 333
Db 338 I-----NRRVEAEVE 347

RESULT 21
US-09-573-630A-2
; Sequence 2, Application US/09573630A
; Patent No. 6713062
; GENERAL INFORMATION:
; APPLICANT: MERCHANT, JUANITA L.
; TITLE OF INVENTION: ACINETOBACTER OUTER MEMBRANE PROTEIN AND GENE SEQUENCE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; FILE REFERENCE: 4100.001700
; CURRENT APPLICATION NUMBER: US/09/573,630A
; CURRENT FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/134,399
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Acinetobacter sp.
US-09-573-630A-2

Query Match      12.4%; Score 226; DB 4; Length 349;
Best Local Similarity 24.5%; Pred. No. 5.8e-14;
Matches 99; Conservative 57; Mismatches 124; Indels 124; Gaps 18;

Qy 3 AIFVLNAPKDNWTYAGGKLGS-----QYHDTGFGYNGFONNNG-----PTRNDQL 49
Db 7 ALAMLVAAP-----FAAANAGVTVPLMLGYTFODTQHNNG---NDGELTSSPELQDDL 58

Qy 50 GAGAFGGYQVNPYLGPFMGYDMLGRMAYKGSVDNGA-----FKAGGVQLTAKLGYPIITDDL 105
Db 59 FVGAAGVVELTPWLGFEEYSQV-----KGDVDAEAGAEYKQNI----- 99
```


Qy 106 DIYTRLGGMVWRADSKGN-YASTGYSRSEHDTGSPVPAGGVENAVTRDIATRLLEYQW-- 162
Db 100 -----AGFYATSDVFTGNYDSKVPYMLLG-----AGHYKIBFEG 135
Qy 163 -----VNNIGDAGTGTDPDNGMLSLGV-----SYRFGQ----- 191
Db 136 VPRGTRGNEEGTLGNAGVGAFWINDALARTTEARGTYHFDEKFWNYTALAGLNVVLGG 195
Qy 192 --EDAAPVAPAP-----APAEVATKHFTLKSVDLVFNFNKATLKPGEQQALDQLYTQ 242
Db 196 RLKPAAPVVEVAPVPPVFPVAPPPQELPEDLNMLRVFFDTNKSNIKQDYKPEIAKVAEK 255
Qy 243 LSNMDPKDGSVAVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAK-GIPAGKISARGWGES 301
Db 256 L--VEYPNATARIEGHTDNTGPRALNERLSLARANSVKSSLVNEYNDASRLSTQGFAMD 313
Qy 302 NPVTGNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVT-OPQA 344
Db 314 QPIADN---NTKEGRAM-----NRRVFATTIGSRTVLAEQVA 348

RESULT 22
US-09-252-991A-19595
; Sequence 19595, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19595
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19595

Query Match 10.9%; Score 199; DB 4; Length 235;
Best Local Similarity 28.4%; Pred. No. 1.6e-11;
Matches 63; Conservative 29; Mismatches 64; Indels 66; Gaps 8;

Qy 125 ASTGYSRSEHDTGSPVPAGGVENAVTRDIATRLLEYQWVNNIGDAGTGTDPDNGMLSLG 184
Db 65 AGLGAISSWAGWALIGGVGAA-----YCVHVGAGEQ----- 99
Qy 185 VSYRFGQEDAAPVAPAP-----APAEVATKHFTLKSVDLVFNFNKATLKPGEQQALD 237
Db 100 -----VAPPPQPVEEVAPPPVVKETIVVDLHFAFDSSKVDAADSEKLN 146
Qy 238 QLYTQLSNMDPKDGSV-----VLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIAGK 292
Db 147 GIAERLK-----GEAASTRLSITGHTDSVGSDAYNQKLSERRANAVANYLIDAGVPSSI 200
Qy 293 I-SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVK 333
Db 201 IVGVQGLGESQPVADN-----KTR-----EGRAENRVERILIK 233

RESULT 23
US-09-328-352-5775
; Sequence 5775, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5775
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5775

Query Match 10.6%; Score 193.5; DB 4; Length 259;
Best Local Similarity 25.1%; Pred. No. 6.4e-11;
Matches 65; Conservative 36; Mismatches 99; Indels 59; Gaps 6;

Qy 80 SVNGAFKAGVQLTA-KLGYPTDLDLDIYTRIGMVMWRADSKGNVASTGVSRSEHDTGV 138
Db 50 TVVGAADVLSGCQTTGNLGGVEYDKAALGTLLIGAAAGYGISKNANSSRQNNRAAIGA 109
Qy 139 SPVPAGGV-----EWAVTRDIATRLLEYQWVNNIGDAGTGTDPDNGMLSLGVSYRFGQED 193
Db 110 VLGAAGSLYLDQKEKKLREQMA-----GTGVEUGRNPDGSV----- 145
Qy 194 AAPVAPAPAPAEVATKHFTLKSVDLVFNFNKATLKPGEQQALDQLYTQLSNMDPKDGS 253
Db 146 -----QLIMPGSITFTDNKSNIKENFYATLTKVAQTLLA--EDNKSAL 185
Qy 254 VLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIAGKISARGMGESNPVTGNTCDNVK 313
Db 186 LVGTGTYDNTGDSINITPLSQARQSVKYLAKGVPSRIDAQGYGSSNPDIADNSTASGR 245
Qy 314 ARAALIDCLAPDRRVEIEV 332
Db 246 EQ-----NRRVELSI 255

RESULT 24
US-09-902-540-15847
; Sequence 15847, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15847
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15847

Query Match 10.5%; Score 191; DB 4; Length 342;
Best Local Similarity 32.3%; Pred. No. 1.7e-10;
Matches 51; Conservative 32; Mismatches 67; Indels 8; Gaps 4;

Qy 188 RFG--QEDAAPVAPAPAPAEVATKHFTLKSVDLVFNFNKATLKPGEQQALDQLYTQLSN 245
Db 172 QFGPPENNGCPYDSP---PYVVVESDRIRKGNVLFETGSAVIQKQSYPLLDVAVTL-R 227
Qy 246 MDPKDGSAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIAGKISARGMGESNPVT 305
Db 228 KNPTLGPVLIEGHTDNRGSPALNWLSDRAKSVLEVLVAKGIARKELSSKGFDFNP 287
Qy 306 GNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTQ 343
Db 288 TNDTALGRANRRVDFRLV--RAELETEKKEVTVVPAGQ 323

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Qy 110 RLGMVWRADSKNGNYASTG-VSRSEHDTGVSVPFAGGVWAVTRDIATRLLEYQWVNNIGD 168
Db 41 -IGSLVG-----AGVGALSSSKHGRGKALIGAAAGAAAGGCGIGYMDVQ-----84
Qy 169 AGTVGTRPDNGMLSLGVSRYFGQEDAAPVVPAPAPAPAEVATKFTLKSDVLEFNFKATL 228
Db 85 -----EAKLRDKMQGTGVSVTRNGDNIV-----LNNPNVVTFDNSGANL 123
Qy 229 KPBGQQALDOLYTLQLSNMDPKDGSAV-VLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKG 287
Db 124 KPAGANTLTGVAMVLKEYEK--TAVNVVGYTDTSGSKDLNMRLSQQRADSVASALITQG 180
Qy 288 IPAGKISARGMGSGSNPVGTGNTCNVKAARALIDCLAPDRVEI 330
Db 181 VAANRIRTTGMGPANPIASNSTAEGRAQ-----NRRVEI 214

RESULT 27
US-08-572-447C-15
; Sequence 15, Application US/08572447C
; Patent No. 5955090
; GENERAL INFORMATION:
; APPLICANT: Knapp, Bernhard
; APPLICANT: Hungerer, Klaus-Dieter
; APPLICANT: Broker, Michael
; APPLICANT: Von Specht, Bernd-Ulrich
; APPLICANT: Domdey, Horst
; TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
; TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/572,447C
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94120023.0
; FILING DATE: 16-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: M. Paul Barker
; REGISTRATION NUMBER: 32,013
; REFERENCE/DOCKET NUMBER: 05552.1395-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 226 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-572-447C-15

Query Match 10.0%; Score 182; DB 2; Length 226;
Best Local Similarity 29.9%; Pred. No. 7.3e-10;
Matches 52; Conservative 27; Mismatches 41; Indels 54; Gaps 6;

Qy 198 VAPAPAPAEVAT-----KHFTLKSDVLEFNFK 225
Db 65 LAAPAPFVADVCSDSNDGVCDNVDKPDTPANVTVDANGCPAAVEVVRVOLDVKFDFK 124

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Qy 226 ATLKPEGQALDOLYQLSNM-----DPKDGSAVLGYTDRIGSBAYNQOLSEKRAQSVV 280
Db 125 SKVK-----ENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAYNQKLSERRANAVR 177
Qy 281 DYLVAK-GIPAGKISARGMGESNPVTGNTCDNVKAAALIDCLAPDRRVEIEVK 333
Db 178 DVLVNEGVGGRNAVGVESRPV-----ADNATAEGRAI-----NRRVEAEVE 222

RESULT 28
US-09-267-747-15
; Sequence 15, Application US/09267747
; Patent No. 6300102
; GENERAL INFORMATION:
; APPLICANT: Knapp, Bernhard
; APPLICANT: Hungerer, Klaus-Dieter
; APPLICANT: Broker, Michael
; APPLICANT: Von Specht, Bernd-Ulrich
; APPLICANT: Domdey, Horst
; TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
; TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins.
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/267,747
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/572,447
; FILING DATE: 14-DEC-1995
; APPLICATION NUMBER: EP 94120023.0
; FILING DATE: 16-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: M. Paul Barker
; REGISTRATION NUMBER: 32,013
; REFERENCE/DOCKET NUMBER: 05552.1395-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 226 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-267-747-15

Query Match 10.0%; Score 182; DB 3; Length 226;
Best Local Similarity 29.9%; Pred. No. 7.3e-10;
Matches 52; Conservative 27; Mismatches 41; Indels 54; Gaps 6;

Qy 198 VAPAPAPAEVAT-----KHFTLKSVDLVLFNFK 225
Db 65 LAPAPEFVADVCDSDNDGVCONVDKCPDTPANVTVDANGCPAFAEVRVQLDVKFDFDK 124
Qy 226 ATLKPEGQALDOLYQLSNM-----DPKDGSAVLGYTDRIGSBAYNQOLSEKRAQSVV 280
Db 125 SKVK-----ENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAYNQKLSERRANAVR 177
Qy 281 DYLVAK-GIPAGKISARGMGESNPVTGNTCDNVKAAALIDCLAPDRRVEIEVK 333

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; GENERAL INFORMATION:
; APPLICANT: Knapp, Bernhard
; APPLICANT: Hungerer, Klaus-Dieter
; APPLICANT: Broker, Michael
; APPLICANT: Von Specht, Bernd-Ulrich
; APPLICANT: Domdey, Horst
; TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
; TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins.
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/267,747
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/572,447
; FILING DATE: 14-DEC-1995
; APPLICATION NUMBER: EP 94120023.0
; FILING DATE: 16-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: M. Paul Barker
; REGISTRATION NUMBER: 32,013
; REFERENCE/DOCKET NUMBER: 05552.1395-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 161 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-267-747-11

Query Match          9.9%; Score 181; DB 3; Length 161;
Best Local Similarity 30.1%; Pred. No. 5.5e-10;
Matches 52; Conservative 26; Mismatches 41; Indels 54; Gaps 6;

Qy 199 APAPAPAEVAT-----KHFLLKSDVLFNFNKA 226
Db 1 APAPEVADVCSDSNDGVCDNVKCPDTPANVTVDANGCPAFAEVVRVQLDVKFDKDS 60

Qy 227 TLKPEGQOALDQLYTQLSNM-----DPKDGSAVVLGYTDRIGSBAYNQOQLSEKRAQSVVD 281
Db 61 KVK-----ENSYADIKNLADFVKQYPSSTTTVEGHTDSVGTDAYNQKLSERRANAVRD 113

Qy 282 YLVAK-GTPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRVEIEVK 333
Db 114 VLVNEYGVGGRVNAVGYGSRPV-----ADNATAEGRAI-----NRRVEAEVE 157

RESULT 31
US-09-252-991A-18046
; Sequence 18046, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18046
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18046

Query Match          9.7%; Score 176.5; DB 4; Length 266;
Best Local Similarity 36.5%; Pred. No. 3.3e-09;
Matches 42; Conservative 23; Mismatches 39; Indels 11; Gaps 3;

Qy 218 DVLFFNFNKATLKPEGQOALDQLYTQLSNMPDKGSAVVLGYTDRIGSBAYNQOQLSEKRAQ 277
Db 148 DVLFDLDKSLDKPGAMRNIOQL-AEFLQNP-ERQVIVEGYTDTSGSANTYQRLSERRAD 205

Qy 278 SVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRVEIEVK 332
Db 206 SVRMALLSRGISPERVATRGVKEYPVASNGTSSGRAM-----NRRVEVTI 251

RESULT 32
US-09-489-039A-13729
; Sequence 13729, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13729
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13729

Query Match          9.6%; Score 175; DB 4; Length 633;
Best Local Similarity 33.0%; Pred. No. 1.7e-08;
Matches 59; Conservative 28; Mismatches 64; Indels 28; Gaps 8;

Qy 168 DAGTVGTRPDNGM---LSLGVSYRFGQEDAAPVV-----APAPAPAEVATKHFLL 215
Db 441 DAALLDSWARNGVPLRLSLGLYH--GEQIRLPLEAIRGVVPPPPPGVQHVAPDVIRL 498

Qy 216 KSDVLFNFNKATLKPEGQOALDQLYTQLSNMPDKG-SAVVLGYTDRIGSBAYNQOQLSEK 274
Db 499 DMSLFDGTGKWLKPGSTK---RLVSLMDIKARPGWLIIVVAGHTDSVGEKANQLLSLK 555

Qy 275 RAQSVVDYLVAKG-IPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRVEIEVK 332
Db 556 RAESVRDWMRDTGDVPDSCFAVOGYGESRPIATN--DTPEGRAL-----NRRVEISL 605

RESULT 33
US-09-252-991A-29681
; Sequence 29681, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
```

[illegible]

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RESULT 37
US-09-267-747-13
; Sequence 13, Application US/09267747
; Patent No. 6300102
; GENERAL INFORMATION:
; APPLICANT: Knapp, Bernhard
; APPLICANT: Hungerer, Klaus-Dieter
; APPLICANT: Broker, Michael
; APPLICANT: Von Specht, Bernd-Ulrich
; APPLICANT: Domdey, Horst
; TITLE OF INVENTION: Immunogenic Hybrid Protein OprP-OprI
; TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins.
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/267,747
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/572.447

```

	Query Match	9.2%	Score 167.5;	DB 4;	Length 344;
	Best Local Similarity	31.5%;	Pred. No. 3.8e-08;		
	Matches	57;	Conservative	26;	Mismatches 65; Indels 33; Gaps 7
Qy	168	DAGTVGTRPONGMLSLGVSYRFG-----QEDAAFPVAPAP--APAPEAVTKHPTLKS--	217		
Db	170	DGDGVVDREACPNEGVAHRGPCBPKEPTPPPAPEPAQAPAPELATQAQTTEAPT	229		
Qy	218	-----DVLNFNFKATLKPGQQALDQLYTLQLSNMDPKDGSAVVL---GYTDRIGSEAYN	268		
Db	230	RLPTEHHVQPVGSTLSDSERRNLDAIDYL-----KANPGVSIRIEGTDTNTGPBELN	284		
Qy	269	QQUSEKRAQSVDVLYAKGIIPAGKISARGMGESNPVTGNTCDNVKARAALTDCLADPRRV	328		
Db	285	RTLSQDRADAVROYLIQQGHSSRLTKAGYGPAOPIASN---DTPEGRSAAAA-----NRRV	335		

Qy 329 E 329
Db 336 E 336

RESULT 39

US-09-902-540-12745
; Sequence 12745, Application US/09902540
; Patent No. 6933447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12745
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-12745

Query Match 9.2%; Score 167; DB 4; Length 409;
Best Local Similarity 33.3%; Pred. No. 5.5e-08;
Matches 39; Conservative 23; Mismatches 43; Indels 12; Gaps 2;

Qy 214 TLKSDVLFNFNKATLKPEGQALDQLYTQLSNMDPKGSVAVLVGYTDRIGSEAYNQOLSE 273
Db 282 TMSGOVLFPASNAVLLPAPRQLTEVAHLK---VSDSPWVIEGHTDSMGSDAMNEALSY 338
Qy 274 KRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEI 330
Db 339 RRAEHVREFLSQGVSRDRIQVRLGELGYRVPVANNSTPEGRAN-----NRRVEI 386

RESULT 40

US-09-252-991A-26245
; Sequence 26245, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26245
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26245

Query Match 9.1%; Score 166.5; DB 4; Length 417;
Best Local Similarity 34.1%; Pred. No. 6.4e-08;
Matches 43; Conservative 22; Mismatches 50; Indels 11; Gaps 3;
Qy 218 DVLNFNFNKATLKPEGQALDQLYTQLSNMDPKGSVAVLVGYTDRIGSEAYNQOLSEKRAQ 277
Db 303 DVLDFNFRAELKPAANRTALKL-VQFLQNFRRVRIE-GYDTSVGRQANLDSLRRERQ 360
Qy 278 SVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKE 337
Db 361 AVADVLADLGVDPARMQVVGYGEAFVFTDNASNRGRAQ-----NRRVEIVFSNDKG 411

Qy 338 VVTQPQ 343
Db 412 QLSAPR 417

RESULT 41

US-09-252-991A-19373
; Sequence 19373, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19373
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19373

Query Match 9.0%; Score 163.5; DB 4; Length 169;
Best Local Similarity 37.5%; Pred. No. 3.2e-08;
Matches 45; Conservative 15; Mismatches 49; Indels 11; Gaps 3;

Qy 213 FTLKSDVLFNFNKATLKPEGQALDQLYTQLSNMDPKGSVAVLVGYTDRIGSEAYNQOLS 272
Db 58 FGMSSKVLFGNLDRLNPDSRNTLTKTARALLAVD--IDKVRLEGHTDNTYGDGEGYNOKLS 115
Qy 273 EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIV 332
Db 116 ERRAESVAAVFRAGMPANIEVRGLGMSKFPADV-----KTRAG-----RSENRRAIVV 166

RESULT 42

US-09-328-352-5824
; Sequence 5824, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5824
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5824

Query Match 8.8%; Score 161; DB 4; Length 278;
Best Local Similarity 34.4%; Pred. No. 1.2e-07;
Matches 44; Conservative 26; Mismatches 52; Indels 6; Gaps 4;

Qy 205 APEVATKHTLKSDVLFNFNK--ATLKPEGQALDQLYTQLSNMDPKGSVAVLVGYTDRI 262
Db 153 APERSTVIADRTASVLPAFDRFDASAIEEGTNSVVKIAEQIKK-SPTTPIIVSGFTDPL 211
Qy 263 GSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCL 322
Db 212 GKFSYNQELSSKRANTVAKLLVRQGVPSRQIQANSQTD-VYKQCSDDNSSQ--LIQCL 269
Qy 323 APDRRVEI 330

Db 285 DDGDGIPDVTVCPTPE-----TFNSQDEDEGCDPDNAHQPPTEAGQPAPAPL 337
Qy 207 -----
Db 338 ALPPAPVTDKGVVSDSLCQTEPDLGDGFEDEGCPDPNDQDGPDAEDQCPLEAET 397
Qy 211 KHFTLSKSVLFNFNKATLKPGSQ--ALDOLY-----TQLSNMDPK 249
Db 398 INGVODDGCGPKGKAQVRVEGARIVLDKVYFGTGQGVILARSHGLLRQVAATLKANPR 457
Qy 250 DGSVVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTC 309
Db 458 ILMVRVEGHTDDQGNMKNLDSQRRARNVAFVLVKEGIAAQRDLDAVGYGEAKPV--DTN 515
Qy 310 DNVKARAALIDCLAPDRRVEIEV 332
Db 516 ETAKGR-----ENRRRVEFNI 531

RESULT 62
US-09-902-540-16615
; Sequence 16615, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16615
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16615

Query Match 6.8%; Score 124.5; DB 4; Length 597;
Best Local Similarity 20.7%; Pred. No. 0.0017;
Matches 55; Conservative 44; Mismatches 126; Indels 41; Gaps 6;

Qy 81 VDNAGFAKQGVLTAKLGYPTDLDIYTRLGMVWRADSKG-NYASTGVSRSEHDTGVS 139
Db 363 LEHGPAARQCGCPIPDQGDVEPDEIDSCSPDPG---PADNRGCPVRDTDGIDNDKDEC 419
Qy 140 PVFAGGV-----EWAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRFQED 193
Db 420 PNEAGPIERNCPESDTDKDGVPNRADESCVNEPGDAKNLG----- 459
Qy 194 AAPVAPAP---APAPEVATKHFTLKSVDLVFNFNKATLKPEGQOALDOLYTQLSNMDPKD 250
Db 460 -----CPLHILPLVEIRPRLVVMGVFPEPTQARIQKESYELLDWV-ARVIREPEI 511
Qy 251 GSAVVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCD 310
Db 512 PLVVVGAHTDDRGFPDDNRRLSQGRABAVRQYLLIGRDIAPERLKAALGYGQERPIDSNATS 571
Qy 311 NVKARAALIDCLAPDRRVEIEVKGK 336
Db 572 NGRENNRVEFLADPQDQKSEGROR 597

RESULT 63
US-09-902-540-16076
; Sequence 16076, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16076
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16076

Query Match 6.8%; Score 124; DB 4; Length 113;
Best Local Similarity 32.5%; Pred. No. 0.00015;
Matches 38; Conservative 16; Mismatches 51; Indels 12; Gaps 3;

Qy 214 TLKSD-VLFNFKATLKPEGQOALDOLYTQLSNMDPKDGSVVLGYTDRIGSEAYNQOLS 272
Db 3 SLSADPVYFELDSATLSPESRDLAQLATGLRERPLT--RVTSGHTCELGTTEYNALG 60
Qy 273 EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVE 329
Db 61 HRRAAVVRDILRNGLVSESSQLSVSGFERPLSD-----AHTEDALRRNRRAE 108

RESULT 64
US-09-540-236-3221
; Sequence 3221, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARI
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3221
; LENGTH: 133
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3221

Query Match 6.7%; Score 121.5; DB 4; Length 133;
Best Local Similarity 30.0%; Pred. No. 0.00034;
Matches 36; Conservative 23; Mismatches 50; Indels 11; Gaps 3;

Qy 219 VLFNFKATLKPEGQOALDOLYTQLSNMDPKDGSVVLGYTDRIGSEA-YNQOLSEKRAQ 277
Db 10 VFEDYKFSFKPOYREEVAKVAQMRLEQCASATIECHASRDSIRSSARYNQLSEARAN 69
Qy 278 SVVDYLVAK-GIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGK 336
Db 70 AVKMSLSNEFGIAPNRLNAVGYGDFRPIAPNTTAEGRAM-----NRRVEAVITGSK 120

RESULT 65
5173294-2
; Patent No. 5173294
; APPLICANT: MURPHY,TIMOTHY F.;APICELLA, MICHAEL A.
; TITLE OF INVENTION: DNA PROBE FOR THE IDENTIFICATION
; OF HAEMPHILIUS INFLUENZAE
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/92,948
; FILING DATE: 08-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 932,872
; FILING DATE: 18-NOV-1986

RESULT 69
US-09-252-991A-26810
; Sequence 26810, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUD
; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26810


```
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12628
; LENGTH: 1255
; TYPE: PR
; ORGANISM: Myxococcus xanthus
US-09-902-540-12628

Query Match
Best Local Similarity 5.7%; Score 104; DB 4; Length 1255;
Matches 77; Conservative 27; Mismatches 143; Indels 66; Gaps 14;

QY 50 GAGAFGGVQNDY-IGFEMGVDLGRMAYKGVNDGAFK-----AOGVLTAKLGYPIITDD 104
Db 487 GGASQGGVQVQYPLPSPGTSVDNSGLYVSPKGLAAGDRIDITGGV-LTVYFGLPELTE 545
QY 105 LDIVYRLGGMWRADSKGNASTGVSRSEHDTGVSPFAGGVEMAV--TRDIATRELYQ- 161
Db 546 VKYVGR-----SSGNEVPAPVVVTADIRTCGPRAALLEGVLVEVRDVAVNTGVDE 596
QY 162 ----WVNNIGDAGTGTTRPDNGMLSLGVSYRFGQEDAAAPVVPAPAPAPAPAEVATKHTLKS 217
Db 597 FQOPLVNEAGDAQOGLMDD-----QAYAF-----QVPSICTREFGALRG 636
QY 218 DVLNFKATLKPEGQQALDQLYTQLSNMDPKGSAVVLGYTDRIG-----SBAY 267
Db 637 VLTYNFNSKLVPRFQADMLPPPSLTGFGP-DGYARV-GGTGPVNTFPQALTLSSAY 694
QY 268 NQQL-----SEKRAQSVVDVLAAGIPAGKISA-----RGMGESNPVTGNTCDNVKARAA 317
Db 695 AEALDVITSSNESALSVDGRIT--IFAGQTSATVQVNAVAPASQVTLTATLGSGTQTA 752
QY 318 LIDCLAPDRRVEI 330
Db 753 TIRVLGADEQPEV 765

RESULT 73
US-09-543-681A-5543
; Sequence 5543, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5543
; LENGTH: 180
; TYPE: PR
; ORGANISM: Proteus mirabilis
US-09-543-681A-5543

Query Match
Best Local Similarity 5.5%; Score 101; DB 4; Length 180;
Matches 35; Conservative 15; Mismatches 55; Indels 6; Gaps 5;

QY 196 PVVAPAPAPAEVATKHF-TLKSD--VLNFKATLKPEGQQALDQLYTQLSNMDPKDGS 252
Db 53 PVTEQGPT-AEELARQLEQLKQTVIVFGPKDYVTSYAQLLD-AHAFLRANP-SVR 109
QY 253 AVVLGYTDRIGSEANQQLSEKRAQSVVDVLAAGIPAGKISARGMGESNP 303
Db 110 ITIEGHADERGTPEYNIALGERANAVRMVYLGKGVSAQDLSIVSYGKEKP 160

RESULT 74
US-08-765-081-7
; Sequence 7, Application US/08765081
```

```
; Patent No. 5798260
; GENERAL INFORMATION:
; APPLICANT: Tarr, P.I., Bilge, S.S., Besser, T.E., Vary Jr., J.C.
; TITLE OF INVENTION: Escherichia Coli 0157:H7 Epithelial Adhesin
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Center, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC compatible/Pentium
; OPERATING SYSTEM: MS-Windows 3.1
; SOFTWARE: Word for Windows-6.0
; CURRENT APPLICATION DATA: US/08/765,081
; APPLICATION NUMBER: US/08/765,081
; FILING DATE: March 26, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06994
; FILING DATE: June 7, 1995
; APPLICATION NUMBER: US 08/265,714
; FILING DATE: June 24, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; REFERENCE/DOCKET NUMBER: CHOR-1-10286
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0718 (direct)
; TELEFAX: 1-206-224-0779
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 663 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: E. coli CirA protein amino acid sequence
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia Coli
US-08-765-081-7

Query Match
Best Local Similarity 5.5%; Score 100.5; DB 1; Length 663;
Matches 55; Conservative 29; Mismatches 77; Indels 63; Gaps 14;

QY 15 TWYAG----GKLWMSQYHDTG--FYNGFQNNNGPTNRNDQLGAGAFGGYQVNPYLGPMG 68
Db 454 SWELGLYMGEGWLEGVSSVTVFRNDVKDRISIRTSDVNAAP--GYQ--NFVGFRTG 509
QY 69 YDWLGRMAYKGSVDN-GAFKAQGVQLTAK-----LCYPITDLDIYT----- 109
Db 510 AN--GRRIPVFSYNNVKNARKQGVETELKIPFNDWKLSINITYNDRGDSVNGENKPLSD 567
QY 110 ---RLGGVMWRADSKGNVASTGVSRSEHDTGVSP-----VFAGGVEMAVTRDIATRELYQW 162
Db 568 LPFHLEADNSFFYSYGHY--TGQRADSATAKTGGYTIWNTGAQWYTKDKVLR---AG 622
QY 163 VNNIGDA---GTGTRPDNGMLS-----LGVSYRF 189
Db 623 VLNLGDKTANGTLDWKPD---LSRDDYSYNEGDRRYFMAVDYRF 663

RESULT 75
US-09-098-082-7
; Sequence 7, Application US/09098082
; Patent No. 6040421
; GENERAL INFORMATION:
; APPLICANT: Tarr, P.I., Bilge, S.S., Besser, T.E., Vary Jr., J.C.
; TITLE OF INVENTION: Escherichia Coli 0157:H7 Epithelial Adhesin
; NUMBER OF SEQUENCES: 12
```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 1.44mb storage
COMPUTER: IBM PC compatible/Pentium II
OPERATING SYSTEM: MS-Windows 95
SOFTWARE: Word for Windows-6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/765,081
FILING DATE: March 26, 1997
APPLICATION NUMBER: PCT/US95/06994
FILING DATE: June 7, 1995
APPLICATION NUMBER: US 08/265,714
FILING DATE: June 24, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: CHOR-1-12402
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
TELEFAX: 1-206-224-0779
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: E. coli CirA protein amino acid sequence
HYPOTHEtical: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia Coli
/US-09-098-082-7

```

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27792
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27792

Query Match 5.5%; Score 100; DB 4; Length 300;
Best Local Similarity 24.6%; Pred. No. 0.16;
Matches 56; Conservative 31; Mismatches 99; Indels 48; Gaps 10;

QY 120 SKGNY-----ASTGVSRSEHDTGSPVPFAGGVEMAVTRDIATLEYQWVNNIGDAGTVGT 174
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 46 NEGKYLSETLTVGVF-NQPDRLSKLPIGDERPRTEPEPTSVSEQPSDAAASADSLR 104
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 175 RPNGMLSLGVSRYRFGQEDAAPVAPAPAPAPVATKHFTHKSDVLF--NFNKATLKPE 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 105 IADS-----VRDAFGD-----LIASDQLSVRGNELWIEITLNSLLFPS 143
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 G-----QQALDQLYTLQSNMDDKGSAAVLGYTD--RIGSEAY--NQQLSEKRAQSVVDY 282
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 144 GDALPNDAAAPDIEVKAKILAPYKNIHVGEFTDDVPIHSPPRYPTNWELSAARAASIVRL 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 283 LVAKGIPAGKISARGGCESNPVTGNTCDNVKAPAAALIDCLAPRRVEIEVKGYKEV 338
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 204 LGNDGVEPSHMAVGYGEFQFV----ADNASAEGR-----AKRRRVVLVIARNLEV 250
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 77
US-09-041-889-30
; Sequence 30, Application US/09041889
; Patent No. 6033864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Cohavy, Offer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Microbial UC PANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/837,058
; FILING DATE: 11-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PM 3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 367 amino acids
; TYPE: amino acid

```

```
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-889-30

Query Match      5.5%; Score 100; DB 3; Length 367;
Best Local Similarity 22.9%; Pred. No. 0.22; Indels 66; Gaps 12;
Matches 54; Conservative 33; Mismatches 83;

Qy 13 DNTWYAGKLGWSQYHDTGFY-----GNGFQ-----NNGPTRNDQL 49
Db 139 DNFMQQRGN-GFATYRNTDFGLVDGLNFVAVQYQKNGNPSGEGFTSGVTNNGRDALRQN 197
Qy 50 GAGAFGGYQVNPYLGFEFG-----YDWLGRMAYKGSVDNGAFKAGQVLTAKLGYPI 101
Db 198 GDGV-GGSITYDYEGFGIGGAISSSKRTDAQNTAAIYGNDRAEITYTGGLKYDANNIYLA 256
Qy 102 TDDLDIY--TRLGGMVWRADSKGNVASTGVSRSSEHDTGSPVFA-----143
Db 257 AQYTQTYNATRVGSLGW-ANKAQNFEA--VAQYQDFGLRPSLAYLQSKGNLGRGYDDE 313
Qy 144 -----GGVEWAVTRDIATRLLEYQWNNIGD---AGTVGTRPDNGMLSLGVSYRF 189
Db 314 DILKYVDVGATYYFNKNMSTYDYK-INLLDDNQFTRDAGINTDN-IVALGLVYQF 367

RESULT 78
US-09-417-264-30
; Sequence 30, Application US/09417264
; Patent No. 6537768
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Microbial UC PANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/417,264
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/041,889
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PM 3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 367 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-417-264-30

Query Match      5.5%; Score 100; DB 4; Length 367;
Best Local Similarity 22.9%; Pred. No. 0.22; Indels 66; Gaps 12;
Matches 54; Conservative 33; Mismatches 83; Indels 66; Gaps 12;
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Qy 13 DNTWYAGKLGWSQYHDTGFY-----GNGFQ-----NNGPTRNDQL 49
Db 139 DNFMQQRGN-GFATYRNTDFGLVDGLNFVAVQYQKNGNPSGEGFTSGVTNNGRDALRQN 197
Qy 50 GAGAFGGYQVNPYLGFEFG-----YDWLGRMAYKGSVDNGAFKAGQVLTAKLGYPI 101
Db 198 GDGV-GGSITYDYEGFGIGGAISSSKRTDAQNTAAIYGNDRAEITYTGGLKYDANNIYLA 256
Qy 102 TDDLDIY--TRLGGMVWRADSKGNVASTGVSRSSEHDTGSPVFA-----143
Db 257 AQYTQTYNATRVGSLGW-ANKAQNFEA--VAQYQDFGLRPSLAYLQSKGNLGRGYDDE 313
Qy 144 -----GGVEWAVTRDIATRLLEYQWNNIGD---AGTVGTRPDNGMLSLGVSYRF 189
Db 314 DILKYVDVGATYYFNKNMSTYDYK-INLLDDNQFTRDAGINTDN-IVALGLVYQF 367

RESULT 79
US-09-543-681A-4908
; Sequence 4908, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4908
; LENGTH: 684
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-09-543-681A-4908

Query Match      5.5%; Score 99.5; DB 4; Length 684;
Best Local Similarity 19.3%; Pred. No. 0.63;
Matches 88; Conservative 50; Mismatches 146; Indels 171; Gaps 20;

Qy 1 MKAIFVLNAPKDNNTWAGGKLGWSQYH--DTGYGNGFQNNNGPTRNDQLGAGAFGGYQ 58
Db 151 MGVINIITKVTKEWHGAVSMGGTLOHNRDAGDSINGDFYLSGPLIEDKLGQLYQ---207
Qy 59 VNPYLGFMGYDWLGRMAY-KGSVDNGAFKAGQVLTAKLGYPTDLDLDIYTRLGGWYVR 117
Db 208 -SSYLRAE-----DKITYGQGRNDN-----KNITAKLAFTPTDNTILLEAG-----248
Qy 118 ADKGNVASTGVSRSSEHDTGSPVFAAG-----VEMAVTR-----152
Db 249 RNSLQRTTTPKSMSEPTN-----RGRLDKNKMLETNNDNHNWALTYKNQFDILHSEL 302
Qy 153 -----DIATRLLEYQW-----VNNIGDAGTVGTRPDNGMLSLGVSYR 188
Db 303 SVYQEQTQKRVQKTEGVDKATGNSKYVEDRREPTINTVFDAKFTAFLPDN-VMTFGGYQ 361
Qy 189 FGQ-EDAAPV-----VAPAPAPEVA-----209
Db 362 YARLKDESSVGGKEVKQKOSTITADQKALFLEDFSVTDNLALTGGRFDDHYYGKHWNPR 421
Qy 210 -----TKHFTLAKSDVLFNFENKATLKEGQQAALDOLYTLQSNMDPKDGSVAVLGYTDRI 262
Db 422 AYAVHLTDEFTIKGGIAKAFAPSLR-----EISPGYGTSTEK-GRIMYGNRDLK 472
Qy 263 GSEAYNQQLSEKRAQSVVDYLVAKGIPAG-----KISARGMGESNPVTG---NTC 309
Db 473 PETSVSQEIG-----VGYDNGDGFTANVTFFNTEFKDKLTNYDTGIDITGLKLYQY 525
Qy 310 DNVKARAALIDCLAPDRRVEIVKGYKEVVTQPOA 344
Db 526 DNVG-----KANIGKIETAVAPFVA 545
```

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RESULT 80
US-09-328-352-6422
; Sequence 830, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6422
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6422

Query Match          5.4%; Score 97.5; DB 4; Length 583;
Best Local Similarity 23.3%; Pred. No. 0.78;
Matches 84; Conservative 43; Mismatches 117; Indels 117; Gaps 22;

Qy      36 GFQNNNG-----PTRNDQLGAGAF-GGY-----QVNP-----YLGFEF--GYD 70
Db      61 GFQYNTVISSATLQEAAGTLVANKPIGAHCLVKGMDQVSPVDGQTYQIGFEMRLPVD 120

Qy      71 WLGRMAYKGSVDNGAFKAQGVQLTAKLGY--PITDDL-DIYTRLGGMVWRADSKGNVAST 127
Db      121 WNGRFLYQG--NGGTDGNLVPATQVSGGGLTNALHDFAVIS-----162

Qy      128 GVSSEHDTGSPVPAGGVE-----WAVTR--DIATRELYQWVNNIGDAGTVGRTP 176
Db      163 --SDAGHNASQNPMP--GLDPQARINYGYGAITKLTTPMAKNLIIKAAYGKLPDRSYAGGTS 218

Qy      177 DNGMLSLGVSRFG-QEADAAPVAPAPAPAEVATKFTLSKSDVLFNFNKATLKPEGQQA 235
Db      219 NGRHAMTAATRLGDQYDG--ILASTFG-----FHLFRA-----A 251

Qy      236 LDQLYT--QLSNM--DPKDGSAVVLGYTDRIGSEAYNQOLSEKR--AQSVVDYLVA-KGI 288
Db      252 AAQLYTAQQLRRVATDENDLSTAL-----TLSEKVKLAKAILDRCDALDGV 297

Qy      289 PAGKI-----SARGMGESNPTGNTCDNVKARAALIDCLAPRRVEIEVKYKEVVTO 341
Db      298 ADGLVQDVESCRTAFDIHKHVPVCSNTRDGTCLSTEQIDVLANTIYRGVPNSAGQALYATQ 357

Qy      342 P 342
Db      358 P 358

RESULT 81
US-09-198-452A-830
; Sequence 830, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffaix, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 830
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-830

Query Match          5.3%; Score 97; DB 4; Length 192;
```

```
Best Local Similarity 25.2%; Pred. No. 0.16;
Matches 29; Conservative 26; Mismatches 50; Indels 10; Gaps 3;

Qy      218 DVLFNFNKATLKPEGQQAALDQLYTQLSNMDPKDGSAAVVLGYTDRIGSEAYNQOLSEKRAQ 277
Db      85 NITPATDSYTIKGBENLAITLNLVHYMKQNP-K-ATLYIEGHTDERGAASYNLALGARRAN 143

Qy      278 SVVDYLVAKGIPAGKISARGMGESNPTGNTCDNVKARAALIDCLAPDRRVEIEV 332
Db      144 AIKEHLRKQGISADRLSTISYGKEHPL--NSGHNELA-----WQONRRTEFKI 189

RESULT 82
US-09-438-185A-783
; Sequence 783, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 783
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0781
US-09-438-185A-783

Query Match          5.3%; Score 97; DB 4; Length 218;
Best Local Similarity 25.2%; Pred. No. 0.2;
Matches 29; Conservative 26; Mismatches 50; Indels 10; Gaps 3;

Qy      218 DVLFNFNKATLKPEGQQAALDQLYTQLSNMDPKDGSAAVVLGYTDRIGSEAYNQOLSEKRAQ 277
Db      111 NITPATDSYTIKGBENLAITLNLVHYMKQNP-K-ATLYIEGHTDERGAASYNLALGARRAN 169

Qy      278 SVVDYLVAKGIPAGKISARGMGESNPTGNTCDNVKARAALIDCLAPDRRVEIEV 332
Db      170 AIKEHLRKQGISADRLSTISYGKEHPL--NSGHNELA-----WQONRRTEFKI 215

RESULT 83
US-09-252-991A-17204
; Sequence 17204, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17204
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
```



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;
; LENGTH: 703 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: E. coli CirA protein amino acid sequence,
; DESCRIPTION: wherein "Xaa" residues represent gaps
; DESCRIPTION: introduced to facilitate best alignment with
; DESCRIPTION: SEQ ID NO:8.
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: ESCHERICHIA COLI
; PCT-US95-06994-9

Query Match          5.2%; Score 95; DB 5; Length 703;
Best Local Similarity 23.4%; Pred. No. 1.8;
Matches 55; Conservative 29; Mismatches 77; Indels 74; Gaps 14;

Qy 15 TWYAG----GKLWMSQYHDTG--FYGNQGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEMG 68
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 483 SWELGLYYMGEGWLEGVESSVTVFRNDVKDRISISRTSDVNAAP--GYQ--NFVGFETG 538

Qy 69 YDWLGRMAYKGSVDN-GAFKAQGVOLTRAK-----LGYPTDLDIYT----- 109
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 539 AN--GRRIPVFSYVNVKARNQGVETELKIPFNDEWKLISINYTYNDGRDVSNGENKPLSD 596

Qy 110 ---BLGGMWVRADSKGNVASTGVSRSEHDTGVSP-----VFAGGVVEWAVTRDIATRLVQW 162
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 597 LPFHLEADNSFYVSGHY--TGQKRADSAATAKTTCGGYTIWNTGAAMQVTKDVKUR---AG 651

Qy 163 VNNTIGDA-----GTGTRPDNGMLS-----LGVSYRFP 189
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 652 VLNLGDKKXXXXXXXXTANGTLDWKFD---LSRDDYSYNEDGRRYFMADVDFR 703

RESULT 87
US-09-489-039A-13005
; Sequence 13005, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13005
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13005

Query Match          5.2%; Score 94; DB 4; Length 182;
Best Local Similarity 33.7%; Pred. No. 0.3;
Matches 29; Conservative 12; Mismatches 41; Indels 4; Gaps 2;

Qy 219 VLFNFKATLKPEGQALDQLYTOL--SNMDPKGSVVLGYTDTRIGSEAYNQQLSEKRAQ 277
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 80 VYFDLKDYRSDFAAMLDAHANFLRNSPSYK---VTVEGHADBERGTPEYNIALGERRAN 136

Qy 278 SVVDYLVAKGIPAGKISARGESNP 303
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 137 AVKMYLOGKGVSAQDIISVSYGKEKP 162

RESULT 88
US-09-328-352-6018
; Sequence 6018, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
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;
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TYPE: amino acid
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6018
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-6018

Query Match          5.2%; Score 94; DB 4; Length 732;
Best Local Similarity 19.5%; Pred. No. 2.4;
Matches 75; Conservative 41; Mismatches 126; Indels 142; Gaps 20;

Qy 39 NNGSP-TRNDQLGAGAFGGYQVNPYLGFEMGYDWLGRMAYKGSVDNG-----AFKAQGVQ 92
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 290 NPNGPIDRSVLIGDPNFGKYEADVY---RTGY-----TFKHTFDNGWNFQNFQVQKTE 340

Qy 93 LTAKLGYPTDLDIYTRLGMVWRADSKGNVASTGVSR----- 132
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 341 MDGKA-----VFARTGSNFWAKDKQGEIDYTTISRKNNSRHOVIDNLSFAIDNRLN 391

Qy 133 -----EHDGTGV----- 159
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 392 KQFDLYGMQHIDINICVDAFQEKSDYTDNDKYDIDGLNIYNPYGQNVTLKQVRDI--NRLK 450

Qy 160 Y-----QWYNNIGDA---GTGTRPDNGML--SLGVSYRFGQE 192
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 451 YLGLYLRDRIQLNDQLLLSLSGRDWAQTQTTSLVTGNASKQSDNAFTGSASVMYTL--ND 509

Qy 193 DAAPVAPAPAPAPAPAVATKHTLKSDVLFNFENKATLKPE--GQALDQLYTQLSNMDDPKDG 251
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 510 IVAPYVSYSATSFTPNSGT-----DVNSNPFPEKPKQV--EVGMKLOSPDQRIQ 556

Qy 252 SAVV-----LGYTDTRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISA----- 295
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 557 GATAWYDLKRONVLVTD--TANNKYKVGQGEQLRGIEETLSAEILEGKLTAATYTYTIDA 615

Qy 296 ---RGMGESNPVTGNTCDNVKARA 316
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 616 EISKDANASN--VGKALDNIPEHA 637

RESULT 89
US-07-828-788A-14
; Sequence 14, Application US/07828788A
; Patent No. 5273746
; GENERAL INFORMATION:
; APPLICANT: PAYNE, JEWEL M.
; APPLICANT: HICKLE, LESLIE A.
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: DAVID R. SALIWANCHIK
; STREET: 2421 N.W. 41st STREET, SUITE A-1
; CITY: GAINESVILLE
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,788A
; FILING DATE: 19920129
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SALIWANCHIK, DAVID R.
```


RESULT 91
US-08-933-891-4
; Sequence 4, Application US/08933891
; Patent No. 6096708
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: No. 6096708el Bacillus thuringiensis Isolate
; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
; TITLE OF INVENTION: No. 6096708el Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,891
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,034
; FILING DATE:
; APPLICATION NUMBER: US/08/210,110
; FILING DATE:
; APPLICATION NUMBER: 07/865,168
; FILING DATE: 09-APR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/451,261
; FILING DATE: 14-DEC-89
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/371,955
; FILING DATE: 27-JUN-89
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, Roman
; REGISTRATION NUMBER: 21,023
; REFERENCE/DOCKET NUMBER: M443.C1.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904)375-8100
; TELEFAX: (904)372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: AIZAWAI
; INDIVIDUAL ISOLATE: PS811
; IMMEDIATE SOURCE:
; LIBRARY: LAMBEDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
; CLONE: 811B
; US-08-933-891-4

Query Match 5.2%; Score 94; DB 3; Length 1165;
Best Local Similarity 23.0%; Pred. No. 4.9;
Matches 78; Conservative 38; Mismatches 111; Indels 112; Gaps 22;

Qy 60 NPYLGFEMGYDW---LGRMAYK--GSDVN-GAFKAQGVQLTAKLGY-----STNQLGLKT 99
Db 375 NPVAGIE-GVEFQNTISRSYKSGPIDSFSELPQDASVSPAIGYSHRLCHATFLERIS 433

Qy 100 -PITDDLDIYTRLGGMV--W--RADSKGNVASTG-----VSRSEHDTGVS-----PVFA 143
Db 434 GP-----RIAGTVFSTWTHRSASPTNEVSPSRITQIPWVKAHTLASGASVKGPGFT 484
Qy 144 GGVEWAVTRDIATRLLEYQWVNNIGDAGTV-----GTRPDN-----GMLSLGVSVRFG 190
Db 485 GG-----DILTR-----NSMGELGTLRVTFGTGRLPQSYVIRFRYASVANRSRGTFRYS 531
Qy 191 QEDAAPVVPAPAPAPAEVATK-----HFTLKSVDLVFNFNKATLKPGEQOALDQLYTQLSNM 246
Db 532 QPPSYGISFPKTMWDAGEPLTSRFAHTTLTPTIFS-----RAQEEFD-LYIQ----- 578
Qy 247 DPKDGSAVLGYTDRIG-----SEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESN 302
Db 579 -----SGV---YIDRIEFIPVTATFEAEYDLERAQKVNALFT-----STNQLGLKT 622
Qy 303 PVTGNTCDNVKARAALID---CLAPDRRVEIEVKGYKEV 338
Db 623 DVTDYHIDQVSNLVACLSDSEFCLEKRELSEKVKHAKRL 661

RESULT 92
US-09-176-320-6
; Sequence 6, Application US/09176320
; Patent No. 6172281
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: PREVENTION OF BT RESISTANCE DEVELOPMENT
; FILE REFERENCE: 021565-052
; CURRENT APPLICATION NUMBER: US/09/176,320
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: PCT/EP90/00905
; EARLIER FILING DATE: 1990-05-30
; EARLIER APPLICATION NUMBER: GB 89401499.2
; EARLIER FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 6
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-09-176-320-6

Query Match 5.2%; Score 94; DB 3; Length 1165;
Best Local Similarity 23.0%; Pred. No. 4.9;
Matches 78; Conservative 38; Mismatches 111; Indels 112; Gaps 22;

Qy 60 NPYLGFEMGYDW---LGRMAYK--GSDVN-GAFKAQGVQLTAKLGY-----STNQLGLKT 99
Db 375 NPVAGIE-GVEFQNTISRSYKSGPIDSFSELPQDASVSPAIGYSHRLCHATFLERIS 433
Qy 100 -PITDDLDIYTRLGGMV--W--RADSKGNVASTG-----VSRSEHDTGVS-----PVFA 143
Db 434 GP-----RIAGTVFSTWTHRSASPTNEVSPSRITQIPWVKAHTLASGASVKGPGFT 484
Qy 144 GGVEWAVTRDIATRLLEYQWVNNIGDAGTV-----GTRPDN-----GMLSLGVSVRFG 190
Db 485 GG-----DILTR-----NSMGELGTLRVTFGTGRLPQSYVIRFRYASVANRSRGTFRYS 531
Qy 191 QEDAAPVVPAPAPAPAEVATK-----HFTLKSVDLVFNFNKATLKPGEQOALDQLYTQLSNM 246
Db 532 QPPSYGISFPKTMWDAGEPLTSRFAHTTLTPTIFS-----RAQEEFD-LYIQ----- 578
Qy 247 DPKDGSAVLGYTDRIG-----SEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESN 302
Db 579 -----SGV---YIDRIEFIPVTATFEAEYDLERAQKVNALFT-----STNQLGLKT 622
Qy 303 PVTGNTCDNVKARAALID---CLAPDRRVEIEVKGYKEV 338
Db 623 DVTDYHIDQVSNLVACLSDSEFCLEKRELSEKVKHAKRL 661

```

; FILE REFERENCE: MA-43CDF2D3
; CURRENT APPLICATION NUMBER: US/09/837,961A
; CURRENT FILING DATE: 2001-04-19
; PRIORITY APPLICATION NUMBER: US 09/521,344
; PRIOR FILING DATE: 2000-03-09
; PRIORITY APPLICATION NUMBER: US 08/933,891
; PRIOR FILING DATE: 1997-09-19
; PRIORITY APPLICATION NUMBER: US 08/356,034
; PRIOR FILING DATE: 1994-12-14
; PRIORITY APPLICATION NUMBER: US 08/210,110
; PRIOR FILING DATE: 1994-03-17
; PRIORITY APPLICATION NUMBER: US 07/865,168
; PRIOR FILING DATE: 1992-04-09
; PRIORITY APPLICATION NUMBER: US 07/451,261
; PRIOR FILING DATE: 1989-12-14
; PRIORITY APPLICATION NUMBER: US 371,955
; PRIOR FILING DATE: 1989-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; ORGANISM: Bacillus thuringiensis
US-09-837-961A-4

Query Match          5.2%; Score 94; DB 4; Length 1165;
Best Local Similarity 23.0%; Pred. No. 4.9;
Matches 78; Conservative 38; Mismatches 111; Indels 112; Gaps 22;

QY      60  NPVLGFMGYDW---LGRWAYK--GSVDN-GAFKAQGVQLTAKLGY----- 99
DB      375 NPVAGIE-GVEPQNTISRSIYRKSGPIDSFSELPQDASVSPAIGYSHRLCHATFLERIS 433
QY      100 -PITDDLDIYTRLGGMV--W--RADSKGNVASTG-----VSRSEHDTGVS---PVFA 143
DB      434 GP-----RIAGTVFQWTHRSASPTNEVSPSRITQIPWKAKHTLASGASVIKGGFT 484
QY      144 GGVEWAVTRDIATRLEYQWVNIGDAGTV-----GTRPDN-----GMLSIGSVYRFG 190
DB      485 GG-----DILTR-----NSMGELGTLRVTFGRLPQSYIIRFRYASVANRSGTFRYS 531
QY      191 QEDAAPVAPAPAPAPEVATK-----HFTLKSDVLFNFNKATLKPEGOQALDOLYTQLSNM 246
DB      532 QPSPYGISPFKTMADAGEPLTSSRFAHTLTPTFTFS-----RAQEBFD-LYIQ----- 578
QY      247 DPKDGSAAVLGYTDRIG-----SEAYNQOLSEKRAQSVYDVLVAKGIPAGKISARGMGESN 302
DB      579 -----SGV---YIDREFTPVTATFAEYDLEAOKVVALFT-----STNQLGLKT 622
QY      303 PVTGNTCDNFKARAALID---CLAPDRRVEIEVKGYKEV 338
DB      623 DVTDYHIDQVSNLVACLSDBEFCLDEKRELSEKVYKAKRL 661

RESULT 95
PCT-US92-11337-14
; Sequence 14, Application PC/TUS9211337
; GENERAL INFORMATION:
; APPLICANT: PAYNE, JEWEL M.
; APPLICANT: HICKLE, LESLIE A.
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID R. SALIWANCHIK
; STREET: 2421 N.W. 41st STREET, SUITE A-1
; CITY: GAINESVILLE
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

RESULT 93

US-09-521-344-4

Sequence 4, Application US/09521344

Patent No. 6573240

GENERAL INFORMATION:

APPLICANT: Payne, Jewel M.

APPLICANT: Sick, August J.

TITLE OF INVENTION: Bacillus thuringiensis Isolate Active Against Lepidopteran Pests, and Genes Encoding No. 6573240el

TITLE OF INVENTION: Lepidopteran Pests, and Genes Encoding No. 6573240el

TITLE OF INVENTION: Lepidopteran-Active Toxins

FILE REFERENCE: MA-43CDFD2

CURRENT APPLICATION NUMBER: US/09/521,344

CURRENT FILING DATE: 2000-03-09

EARLIER APPLICATION NUMBER: US 08/933,891

EARLIER FILING DATE: 1997-09-19

EARLIER APPLICATION NUMBER: US 08/356,034

EARLIER FILING DATE: 1994-12-14

EARLIER APPLICATION NUMBER: US 08/210,110

EARLIER FILING DATE: 1994-03-17

EARLIER APPLICATION NUMBER: US 07/865,168

EARLIER FILING DATE: 1992-04-09

EARLIER APPLICATION NUMBER: US 07/451,261

EARLIER FILING DATE: 1989-12-14

EARLIER APPLICATION NUMBER: US 07/371,955

EARLIER FILING DATE: 1989-06-27

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 1165

TYPE: PRT

ORGANISM: Bacillus thuringiensis

US-09-521-344-4

Query Match 5.2%; Score 94; DB 4; Length 1165;

Best Local Similarity 23.0%; Pred. No. 4.9;

Matches 78; Conservative 38; Mismatches 111; Indels 112; Gaps 22;

QY 60 NPYLGFEMGYDW---LGRMAYK--GSVDN-GAPKAGVOL-TAKLGY----- 99

DB 375 NPVAGIE-GVEFQNTISIRYKSGPIDSEFSELPPODASVSPAIGYSHRLCHATFLERIS 433

QY 100 -PITDLDLDIYTRLGMV--W--RADSKGNAYSTG-----VSRSEHDTGVS-----PVFA 143

DB 434 GP-----RIAGTVFSTWTHRSPTNEVSPSRITQIPWVKAHTLASCASVTKGPGFT 484

QY 144 GGVWAVTRDTIATRELYQWNNIGDGTV-----GTRPDN-----GMLSLGVSVRFG 190

DB 485 GG-----DILTR-----NSMGELGTLRTVTGRLPQSYIRFRYASVANRSGTFRYS 531

QY 191 QEDAAPVAPAPAPAEVATK---HFTLKSDVLEFNKATLKPEGOALDQLYTQLSNM 246

DB 532 QPPSVGISFPKTMDEPLUTSRSPAHTTLFTPTIFS-----RAQEEFD-LYIQ----- 578

QY 247 DPKDGSAVVLGYTDTRIG-----SEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESN 302

DB 579 -----SGV---YIDRIEFTPVATPEAYDLERAQKVVALFT-----STNQLGLKT 622

QY 303 PVTGNTCDNVKARAALID---CLAPDRRVEIEVKGKEV 338

DB 623 DVTDYHIDQVSNLVACLSDSEFCLEKRELSEKVKHAKRL 661

RESULT 94

US-09-837-961A-4

Sequence 4, Application US/09837961A

Patent No. 6737273

GENERAL INFORMATION:

APPLICANT: Payne, Jewel

APPLICANT: Sick, August J.

TITLE OF INVENTION: No. 6737273el Bacillus thuringiensis Isolate Active Against Lepidopteran Pests, and Genes Encoding No. 6737273el Lepidopteran-Active Toxins

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11337
FILING DATE: 19921231
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 97/828,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: AIZAWAI
INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
CLONE: 811B
PCT-US92-11337-14

Query Match 5.2%; Score 94; DB 5; Length 1165;
Best Local Similarity 23.0%; Pred. No. 4.9;
Matches 78; Conservative 38; Mismatches 111; Indels 112; Gaps 22;
QY 60 NPYLGFEMGYDW---LGRMAYK--GSVDN-GAFKAQGVOLTAQGY----- 99
DB 375 NPVAGIE-GVEFQNTISRSYRKSGPIDSPQDASVPAIGYSHRLCHATFLERIS 433
QY 100 -PITDDLDIYTRLGGMV--W--RADSKGNVASTG-----VSRSEHDTGVS---PVFA 143
DB 434 GP-----RIAGTVFSWTHRSASPTNEVSPSRITQIPWKAHTLASGASVIKGGPFT 484
QY 144 GGVEWAVTRDIATRLQYQWNNIGDAGTV-----GTRPDN-----GMLSLGVSYRFG 190
DB 485 GG-----DILTR-----NSMGLGTLRVFTTGRLPQSYIIRFRYASVANRSGTFRYS 531
QY 191 QEDAAPVVAPAPAPAEVATK---HFTLKSVDLVFNFNKATLKPEGQOALDQLYTQLSNM 246
DB 532 QPPSYGISFPKTMDSAGEPLTSRFAHTTLFTPTIFS-----RAQBEFD-LYIQ----- 578
QY 247 DPKGSVAVLGYTDRIQ-----SEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESN 302
DB 579 -----SGV-----YIDRIEIPVTPATFEAYDLERAQKVNALFT-----STNQLGLKT 622
QY 303 PVTGNTCDNVKARAALID---CLAPDRRVEIEVKGYKEV 338
DB 623 DVTDYHIDQVSNLVACLSDFECLDEKRELSEKVKHAKEL 661

RESULT. 96
5188960-4
Patent No. 5188960
APPLICANT: PAYNE, JEWEL, SICK, AUGUST J.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE
AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL
LEPIDOPTERAN-ACTIVE TOXINS
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/451,261

FILING DATE: 14-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 371,955
FILING DATE: 27-JUN-1989
SEQ ID NO:4:
LENGTH: 1165
5188960-4

Query Match 5.2%; Score 94; DB 6; Length 1165;
Best Local Similarity 23.0%; Pred. No. 4.9;
Matches 78; Conservative 38; Mismatches 111; Indels 112; Gaps 22;
QY 60 NPYLGFEMGYDW---LGRMAYK--GSVDN-GAFKAQGVOLTAQGY----- 99
DB 375 NPVAGIE-GVEFQNTISRSYRKSGPIDSPQDASVPAIGYSHRLCHATFLERIS 433
QY 100 -PITDDLDIYTRLGGMV--W--RADSKGNVASTG-----VSRSEHDTGVS---PVFA 143
DB 434 GP-----RIAGTVFSWTHRSASPTNEVSPSRITQIPWKAHTLASGASVIKGGPFT 484
QY 144 GGVEWAVTRDIATRLQYQWNNIGDAGTV-----GTRPDN-----GMLSLGVSYRFG 190
DB 485 GG-----DILTR-----NSMGLGTLRVFTTGRLPQSYIIRFRYASVANRSGTFRYS 531
QY 191 QEDAAPVVAPAPAPAEVATK---HFTLKSVDLVFNFNKATLKPEGQOALDQLYTQLSNM 246
DB 532 QPPSYGISFPKTMDSAGEPLTSRFAHTTLFTPTIFS-----RAQBEFD-LYIQ----- 578
QY 247 DPKGSVAVLGYTDRIQ-----SEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESN 302
DB 579 -----SGV-----YIDRIEIPVTPATFEAYDLERAQKVNALFT-----STNQLGLKT 622
QY 303 PVTGNTCDNVKARAALID---CLAPDRRVEIEVKGYKEV 338
DB 623 DVTDYHIDQVSNLVACLSDFECLDEKRELSEKVKHAKEL 661

RESULT 97
5188960-4
Patent No. 5188960
APPLICANT: PAYNE, JEWEL, SICK, AUGUST J.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE
AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL
LEPIDOPTERAN-ACTIVE TOXINS
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/451,261
FILING DATE: 14-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 371,955
FILING DATE: 27-JUN-1989
SEQ ID NO:4:
LENGTH: 1165
5188960-4

Query Match 5.2%; Score 94; DB 6; Length 1165;
Best Local Similarity 23.0%; Pred. No. 4.9;
Matches 78; Conservative 38; Mismatches 111; Indels 112; Gaps 22;
QY 60 NPYLGFEMGYDW---LGRMAYK--GSVDN-GAFKAQGVOLTAQGY----- 99
DB 375 NPVAGIE-GVEFQNTISRSYRKSGPIDSPQDASVPAIGYSHRLCHATFLERIS 433
QY 100 -PITDDLDIYTRLGGMV--W--RADSKGNVASTG-----VSRSEHDTGVS---PVFA 143
DB 434 GP-----RIAGTVFSWTHRSASPTNEVSPSRITQIPWKAHTLASGASVIKGGPFT 484
QY 144 GGVEWAVTRDIATRLQYQWNNIGDAGTV-----GTRPDN-----GMLSLGVSYRFG 190
DB 485 GG-----DILTR-----NSMGLGTLRVFTTGRLPQSYIIRFRYASVANRSGTFRYS 531
QY 191 QEDAAPVVAPAPAPAEVATK---HFTLKSVDLVFNFNKATLKPEGQOALDQLYTQLSNM 246

Db 532 QPSPYGISFPKTMADAGEPLTSRFAHTLFTPTIFS-----RAQEEFD-LYIQ----- 578
Qy 247 DPKQGSVAVLVGYTDRIQ-----SEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESN 302
Db 579 -----SGV---YIDRIEIPVTATPEAEYDLERAKVVALFT-----STNQLGLKT 622
Qy 303 PVTGNTCDNVKARAALID---CLAPDRRVEIEVKYKEV 338
Db 623 DVTYDHIDQVSNLVAACLSDEFCLDEKRELSKVKHAKRL 661

RESULT 98

US-09-902-540-11125
; Sequence 11125, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11125
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11125

Query Match 5.1%; Score 93.5; DB 4; Length 340;
Best Local Similarity 24.9%; Pred No. 0.86;
Matches 65; Conservative 27; Mismatches 118; Indels 51; Gaps 11;
Qy 73 GRMAYKGSVDNGAFKQAQ-GVQLTAKLGYPITDDLDIYTRLGGMVVRAD-----SKGNYA 125
Db 84 GRFRYEGALTVRFPDAESGV-----PLSFDTELYGTGLDVRKEDVDVAARLRFLV 136
Qy 126 STGVSRSE-----HDTGSPVPAGGVEMAVTRDIATRLLEYQVWNNIGDAGTGTGTRP-DNGM 180
Db 137 SRPAKRAELTVLMDTG-KKAFEGEYPPFGEAG-GTPELTPAABRGVMKISLRAFDTAE 194
Qy 181 LSLGVSRYRFGEDA-----APVAPAPAPAPAVATKHTLKSDFLNFENKATLKPEGQ 233
Db 195 FYTGVDLYPWQVDIPHEEVNFASGQADIPATERGKLDKSHALIVDALTKY-----GR 246
Qy 234 QALDQLYTQLSNMDPKQGSVAVLVGYTDRIQSEAYNQQLSEKRAQSVVDYLVAKGIPAGKI 293
Db 247 FASLRLY-----VMGHTDTVGAAGAAENLDLSVRRAKSLAAYFRKKGLRV-PV 291
Qy 294 SARGMGESNPVTGNTCDNVKA 314
Db 292 YYEGLGEEAPAVATPDTEAE 312

RESULT 99

US-09-543-681A-7665
; Sequence 7665, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7665

; LENGTH: 417
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7665
Query Match 5.1%; Score 93.5; DB 4; Length 417;
Best Local Similarity 22.4%; Pred. No. 1.2; Indels 85; Gaps 13;
Matches 66; Conservative 33; Mismatches 110;
Qy 68 GYDMLGRMAYKGSVDNGAF-----KAQVQLTAKLGYPITDDLDIYTRLG 112
Db 87 GADYANVQPHSGSQANAAYMALLKPGDVTGLGNLAQGGHLTH--GSPVNSGKLYNIVP 144
Qy 113 GMVWRADSKGNVASTGVSREHD-----TGVSVPAGGVEMAVTRDIATRLLEYQVWNNIGD 168
Db 145 YGIDEA-GKIDYQDIAEQAKKHKPMIIGGFSAYSLVDWAKMREIA-----DSVGA 195
Qy 169 AGTVGTRPDNGLSLGVSRYRFGQEDAAPVAPAPAPAPAV-----ATKHFTLKSDFLNFNKA 226
Db 196 YLFVDMAHVAGMIAAG-----VYENPVPHAHVVTTHTKTLAG----- 233
Qy 227 TLKPEGQAL-----DQLYTQLSN-----MDPKQGSVAVLVGYTDRIQSEAYNQ 270
Db 234 ---PRGGLILAKGGDEBFYKLNLSAVFPSSGQGLMHVIAGKAVALKAMEPEFKVYQQ 290
Qy 271 LSEKRAQSVVDYLVAKGIPAGKISARGMGE-----SNPVTGNTCDNVKARA 316
Db 291 VA-KNAKAMVDVFLARGY---KVVSGGTENHLFLDLVDKIDITGKDADAALGRA 340

RESULT 100

US-08-714-741-32
; Sequence 32, Application US/08714741
; Patent No. 6500613
; GENERAL INFORMATION:
; APPLICANT: Briles, David E. S.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
; TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
; TITLE OF INVENTION: PORTIONS AND PRODUCTS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.
; ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,741
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2460
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 8991 amino acids

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;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: amino acid
US-08-714-741-32

Query Match      5.1%; Score 93.5; DB 4; Length 8991;
Best Local Similarity 24.8%; Pred. No. 1.2e+02;
Matches 50; Conservative 21; Mismatches 72; Indels 59; Gaps 8;

Qy 177 DNGMLSLGVSYRFGQEDAAPVAPAPAPAPE--VATKHFTLKSDVLFN-----FNKATL 228
Db      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 7918 DYARRSGEYNNRFPOQPPKAEKDPAPKPEQVPAPKTLILKAKLAGAKSKAATKKAEL 7977
Db      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

Qy 229 KPEGQOALDQLYTQLSNMDPKDGSNAVVLGYT-DRIGSEAYNQQLSEK----- 274
Db      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 7978 EPELEKAEAELENLLSTLDPE-----GKTQDELDKAEAEAELENKKVEALPNQVSELEE 8030
Db      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

Qy 275 -----RAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCL 322
Db      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 8031 ELSKLEDNLKDAETNNVEDY-KEGLEAEAIATKQAELEKTP-----KELDAALNEL 8080
Db      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

Qy 323 APDRRVEIEVKGYKEVWTQPOA 344
Db      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 8081 GPD-----GDEETPPPEA 8094
Db      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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Search completed: September 20, 2005, 21:40:10
Job time : 51 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2005, 21:25:08 ; Search time 167 Seconds
(without alignments)
796.680 Million cell updates/sec

Title: US-09-647-309a-2
Perfect score: 1822
Sequence: 1 MKALFVLNAAPKONTWTAGG.....DRRVEIEVKGYKVVTPQQA 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1822	100.0	344	2	AAY44077 K.pneumon
2	1822	100.0	344	4	AAG67743 Amino aci
3	1822	100.0	344	4	AAB84122 Amino aci
4	1818	99.8	344	2	AAR93797 Protein L
5	1818	99.8	452	4	AAB67771 Amino aci
6	1813	99.5	344	3	AB18994 A P40 pol
7	1813	99.5	344	3	AB08317 An outer
8	1813	99.5	344	3	AAY93341 Amino aci
9	1813	99.5	344	3	AB08825 A P40 pol
10	1813	99.5	344	3	AB18804 A Klebsie
11	1813	99.5	344	3	AB08341 An outer
12	1813	99.5	344	4	AAG67698 Amino aci
13	1813	99.5	344	4	AAB67770 Amino aci
14	1813	99.5	344	5	AAM48395 Klebsiell
15	1813	99.5	344	5	AAM47796 Klebsiell
16	1813	99.5	344	8	ADI00532 Klebsiell
17	1813	99.5	344	8	ADI56807 K. pneumo
18	1813	99.5	344	8	ADI38366 K. pneumo
19	1781	97.7	385	7	ABO60934 Klebsiell
20	1771	97.2	335	2	AAR8257 K.pneumon
21	1771	97.2	335	2	AAR95644 Klebsiell
22	1771	97.2	335	2	AAR93796 Protein P
23	1294	71.0	369	6	ABM69278 Phototab
24	1279	70.2	384	2	ADF07637 Bacterial
25	1026	56.3	188	2	AAR93798 Protein L

Aar95645	Klebsiell	179	54.0	984	26
Abb83156	Partial O	137	38.2	696	27
Aam50724	Haemophil	344	5	696	28
Aam50721	Haemophil	344	5	688	29
Aae17872	Sequence	153	37.7	687	30
Aam50718	Haemophil	344	5	685	31
Aam50719	Haemophil	344	5	684	32
Aam50717	Haemophil	344	5	684	33
Aam50716	Haemophil	344	5	684	34
Aam50722	Haemophil	344	5	684	35
Aam50725	Haemophil	344	5	683	36
Aam50720	Haemophil	341	5	680.5	37
Aam50723	Haemophil	341	5	680.5	38
Aam50726	Haemophil	341	5	680.5	39
Aam50727	Haemophil	344	5	678	40
AAB44588	Virulence	364	37.2	671	41
ABP54540	Actinobac	364	36.8	671	42
Aay97899	Actinobac	364	36.6	667	43
Aay96097	Actinobac	364	36.6	667	44
Aar62294	Non-typab	359	36.0	655.5	45
ABG80420	Haemophil	353	35.6	649.5	46
AB47447	MOMP P5	353	35.6	649.5	47
AB44589	Virulence	369	35.5	646.5	48
ABP54541	Actinobac	369	35.5	646.5	49
Aay97900	Actinobac	369	35.1	639.5	50
Aay96098	Actinobac	369	35.1	639.5	51
ADM20161	Protein e	157	35.0	638	52
Aar85450	Nontypabl	338	32.2	586.5	53
Aar37423	Tripartit	412	29.4	535.5	54
Aar95646	Klebsiell	72	20.8	379	55
Aar95647	Klebsiell	53	15.4	281	56
ABG91067	Neisseria	236	14.4	262	57
ABP80776	N. gonorr	236	14.4	262	58
ABG80415	Neisseria	242	14.0	255	59
ADP08212	Neisseria	242	14.0	255	60
ADP94937	P. fluore	317	13.8	251	61
ABM94937	Protein a	326	13.4	243.5	62
ADA33932	Actinobac	379	13.3	242.5	63
ADF29221	Bacterial	272	13.3	242	64
ADG32432	Pasteurel	272	13.2	242	65
Adm94951	OprF-CBD	370	12.7	240.5	66
ABP2053	Outer mem	350	12.7	231.5	67
ABM9179	Protein a	350	12.7	231.5	68
ABO81348	Pseudomon	351	12.7	231.5	69
ADM46159	Actinobac	349	12.4	226	70
ADM94953	OprF-CBD	370	12.2	222.5	71
ADH12853	Francisel	393	11.9	216	72
ABM9182	C.jejuni	287	11.5	209	73
ABO70849	Pseudomon	287	11.3	206.5	74
ADA34488	Actinobac	235	10.9	199	75
AAY34500	Porphorym	259	10.6	193.5	76
AAY34373	Porphorym	672	10.6	193.5	77
AAY34373	Porphorym	672	10.6	193.5	78
ABO67662	Klebsiell	566	10.1	184.5	79
ABO64495	Klebsiell	226	10.0	182	80
AAR96627	P. aerugi	220	10.0	182	81
AAR96625	P. aerugi	161	9.9	181	82
AAY34487	Porphorym	223	9.9	180	83
AAY34362	Porphorym	230	9.9	180	84
ADG15029	Pseudomon	261	9.7	176.5	85
ABO69300	Pseudomon	266	9.7	176.5	86
Aau09397	Soluble P	390	9.7	176	87
AAB59178	C.coli Ca	326	9.6	175.5	88
Aay34490	Porphorym	391	9.6	175.5	89
AAY34365	Porphorym	395	9.6	175.5	90
ABO67212	Klebsiell	633	9.6	175	91
ABU41527	Protein e	229	9.6	175	92
Aaw23592	H. pylori	179	9.5	173.5	93
ABO80935	Pseudomon	272	9.5	173.5	94
AB61911	R. anatip	387	9.5	173.5	95
Aaw23591	H. pylori	144	9.4	171	96
ABO68866	Pseudomon	753	9.4	171	97
ADA35583	Actinobac	472	9.3	170	98

99	169.5	9.3	375	7	ADH52744	Adh52744	Porphyrrom	172	112	6.1	207	8	ADH12902	Adh12902	Franciseel
100	169	9.3	179	2	AAW89882	AAw89882	Expressed	173	111.5	6.1	699	8	ADS26420	AdS26420	Bacterial
101	169	9.3	179	4	AAW46316	Abw46316	H. pylori	174	109	6.0	195	7	ADG30762	Adg30762	Streptocpir
102	169	9.3	179	4	ABR82766	ABr82766	H. pylori	175	109	6.0	347	5	ABP30886	Abp30886	Streptococo
103	168.5	9.2	214	2	RAAR9626	AAr9626	P. aerugi	176	109	6.0	347	5	ABP29678	Abp29678	Streptococo
104	168	9.2	395	7	ADH52749	Adh52749	Porphyrrom	177	109	6.0	370	5	ABP25842	Abp25842	Streptococo
105	167.5	9.2	375	7	ADH52741	Adh52741	Porphyrrom	178	106.5	5.8	218	5	AAU97298	Aau97298	Agrobacte
106	166.5	9.1	417	7	ABO77499	AbO77499	Pseudomon	179	106.5	5.8	915	6	ABM70345	Abm70345	Phototrab
107	165.5	9.1	453	2	AAW73918	AAw73918	CD protei	180	105.5	5.8	1124	7	ABO78064	AbO78064	Pseudomon
108	163.5	9.1	453	5	ABG80429	ABg80429	Moraxella	181	105	5.8	275	5	ABBA49871	ABb49871	Listeria
109	163.5	9.0	169	7	ABO70627	ABO70627	Pseudomon	182	105	5.8	453	7	ABO71899	ABO71899	Pseudomon
110	162.5	8.9	179	2	AAW20394	AAw20394	H. pylori	183	104	5.7	699	6	AAU31707	Aau31707	Protein e
111	162.5	8.9	179	2	AAW24651	AAw24651	H. pylori	184	104	5.7	699	6	AAU08471	Aau08471	F. balust
112	162.5	8.9	187	2	AAW20795	AAw20795	H. pylori	185	104	5.7	743	6	ADA33786	Ada33786	Acinetoba
113	161	8.8	278	6	ADA34537	Ada34537	Acinetoba	186	103	5.7	1074	4	ABG24648	ABg24648	Novel hum
114	160	8.8	396	4	AAU41956	AAu41956	Propionib	187	103	5.7	1124	4	ABB59241	ABb59241	Novel hum
115	160	8.8	396	6	ABM38475	ABm38475	Propionib	188	103	5.7	1325	4	AAG98256	AAg98256	Escherich
116	158	8.7	231	2	AAW89813	AAw89813	Protein e	189	102	5.6	167	6	ABMG6997	ABmG6997	Phototrab
117	158	8.7	257	6	ADA35334	Ada35334	Acinetoba	190	101.5	5.6	1510	7	ADG30698	Adg30698	Xanthomon
118	152	8.3	224	4	AAW20105	AAb20105	Moraxella	191	101	5.5	180	7	ADF05258	Adf05258	Bacterial
119	152	8.3	224	5	ABG80432	ABg80432	Moraxella	192	100	5.5	300	7	ABO79046	ABO79046	Pseudomon
120	150	8.2	349	7	ADH52748	Adh52748	Porphyrrom	193	100	5.5	367	2	AAAY42549	AAy42549	E. coli w
121	150	8.2	382	7	ADH52745	Adh52745	Porphyrrom	194	100	5.5	367	2	AAAY34058	AAy34058	E. coli o
122	149	8.2	231	8	ADL06141	AdL06141	M. catarr	195	100	5.5	367	2	AAAY57356	AAy57356	E. coli o
123	147	8.1	550	4	ABBS2692	ABb52692	Escherich	196	99.5	5.5	684	7	ADF04623	Adf04623	Bacterial
124	147	8.1	550	4	ABBS2693	ABb52693	Escherich	197	99	5.4	367	5	ABB08211	ABb08211	Escherich
125	146.5	8.0	172	3	AAAY5091	AAy5091	M. catarr	198	98.5	5.4	188	7	ADD43878	AdD43878	Chlamydia
126	144	7.9	34	5	ADK36418	Adk36418	Novel hum	199	98.5	5.4	214	2	AAAY37603	AAy37603	Chlamydia
127	143.5	7.9	172	3	RAY55092	AAy55092	M. catarr	200	98.5	5.4	214	5	ABG91055	ABg91055	Chlamydia
128	142.5	7.8	152	8	ADL05504	AdL05504	M. catarr	201	98.5	5.4	320	2	AAW27717	AAw27717	S. marces
129	142.5	7.8	172	3	AAAY55090	AAy55090	M. catarr	202	98.5	5.4	320	2	AAW27718	AAw27718	S. marces
130	142.5	7.8	382	7	ADH52743	Adh52743	Porphyrrom	203	98.5	5.4	663	8	ADK13827	AdK13827	E. coli i
131	140.5	7.7	225	6	ABP76748	ABp76748	N. gonorr	204	98.5	5.4	866	6	ABU15381	ABu15381	Protein e
132	140.5	7.7	240	6	ABP80680	ABp80680	N. gonorr	205	97.5	5.4	583	6	ADA35135	Ada35135	Acinetoba
133	139.5	7.7	228	5	AAO17571	AAo17571	M. catarrh	206	97.5	5.4	1683	4	ABG24799	ABg24799	Novel hum
134	139.5	7.7	551	6	AAO16289	AAo16289	Moraxella	207	97.5	5.4	4130	8	ADQ26346	AdQ26346	Chromobac
135	139.5	7.7	553	5	ABG80430	ABg80430	Moraxella	208	97	5.3	192	2	AAAY35412	AAy35412	Chlamydia
136	137	7.5	314	7	ABO70854	ABO70854	Pseudomon	209	97	5.3	192	4	AAE04322	AAe04322	Chlamydia
137	136.5	7.5	172	3	AAAY5089	AAy5089	M. catarr	210	97	5.3	192	4	ABB90544	ABb90544	Chlamydia
138	136.5	7.5	552	8	ADL04924	AdL04924	M. catarr	211	97	5.3	419	4	AAW70788	AAw70788	Chlamydia
139	136	7.5	104	2	AAW89983	AAw89983	Expressed	212	97	5.3	1083	4	ABG25711	ABg25711	Novel hum
140	135	7.4	187	7	ABO80836	ABO80836	Pseudomon	213	96.5	5.3	452	6	ABU47241	ABu47241	Protein e
141	133	7.3	380	5	AAU09198	AAu09198	Soluble p	214	96.5	5.3	4076	6	ABM68692	ABm68692	Phototrab
142	133	7.3	380	7	ABW00418	ABw00418	Porphyrrom	215	96	5.3	117	7	ABO68458	ABO68458	Pseudomon
143	133	7.3	385	2	AAAY34491	AAy34491	Porphyrrom	216	96	5.3	513	2	AAAR04585	AAr04585	Aquaricin
144	133	7.3	385	7	ABW00417	ABw00417	Porphyrrom	217	96	5.3	513	2	AAAR13181	AAr13181	T.aquatic
145	133	7.3	387	2	RAY34366	AAy34366	Porphyrrom	218	96	5.3	513	2	AAAR67653	AAr67653	Aqualysin
146	132	7.2	166	7	ABO65207	ABO65207	Klebsiell	219	96	5.3	847	6	ABU31210	ABu31210	Protein e
147	132	7.2	646	6	ABM70679	ABm70679	Phototrab	220	95.5	5.2	510	5	ABB47606	ABb47606	Listeria
148	131.5	7.2	195	6	ADA35023	Ada35023	Acinetoba	221	95.5	5.2	1787	5	ABBA49791	ABb49791	Listeria
149	130.5	7.2	315	4	ABG17777	ABg17777	Novel hum	222	95	5.2	273	6	ADA35029	Ada35029	Acinetoba
150	128.5	7.1	316	7	ADH52746	Adh52746	Porphyrrom	223	95	5.2	366	6	ABU17811	ABu17811	Protein e
151	127.5	7.0	197	5	AAO17565	AAo17565	M. catarrh	224	95	5.2	429	6	ABU38837	ABu38837	Protein e
152	127.5	7.0	323	7	ADH52747	Adh52747	Porphyrrom	225	95	5.2	431	7	ABO84373	ABO84373	Pseudomon
153	126	6.9	153	1	AAAP82947	AAp82947	16500 dal	226	95	5.2	873	6	ABU23144	ABu23144	Protein e
154	126	6.9	153	1	AAAP80593	AAp80593	16500 dal	227	94.5	5.2	1121	7	ADF75895	Adf75895	Acidothor
155	123.5	6.8	2799	6	ABU37640	ABu37640	Protein e	228	94.5	5.2	1121	7	ADF75895	Adf75895	Acidothor
156	121.5	6.7	133	8	ADL05535	AdL05535	M. catarr	229	94.5	5.2	3896	8	ADL39291	AdL39291	S. hygro
157	121.5	6.7	366	7	ADH52742	Adh52742	Porphyrrom	230	94	5.2	182	7	ABO66488	ABO66488	Klebsiell
158	120.5	6.6	350	5	ABP25843	ABp25843	Streptoco	231	94	5.2	417	6	AAU34661	Aau34661	E. coli c
159	120.5	6.6	350	5	ABG66912	ABg66912	Streptoco	232	94	5.2	417	6	AAU28717	Aau28717	Protein e
160	120.5	6.6	350	8	ADR83934	Adr83934	S. pyogen	233	94	5.2	683	7	ADM07079	Adm07079	Aspergill
161	120	6.6	153	2	AAAR05797	AAr05797	PBOMP-1 g	234	94	5.2	732	6	ADA34731	Ada34731	Acinetoba
162	120	6.6	153	2	AAAS1161	AAa51161	Outer mem	235	94	5.2	735	7	ADM07030	Adm07030	Aspergill
163	120	6.6	153	5	ABG80422	ABg80422	Haemophil	236	94	5.2	891	2	AAAY34495	AAy34495	Porphorym
164	120	6.6	153	5	ABG80421	ABg80421	Haemophil	237	94	5.2	899	2	AAAY34369	AAy34369	Porphorym
165	119	6.5	153	2	AAAR07145	AAr07145	16.6kD ou	238	94	5.2	1165	2	AAAR08200	AAr08200	bt4 Proto
166	117	6.4	330	5	ABG66917	ABg66917	Streptoco	239	94	5.2	1165	2	AAAR39756	AAr39756	Delta end
167	117	6.4	330	5	ABG66916	ABg66916	Streptoco	240	94	5.2	1165	2	AAAR72481	AAr72481	bt4 proto
168	117	6.4	330	5	ABG66915	ABg66915	Streptoco	241	94	5.2	1165	2	AAAR72481	AAr72481	bt4 proto
169	115	6.3	583	6	ABM69481	ABm69481	Phototrab	242	94	5.2	1531	8	ADO57586	AdO57586	Actinobac
170	114	6.3	153	1	AAAP80665	AAp80665	Sequence	243	94	5.2	2013	7	ADF30782	Adf30782	Soil meta
171	112	6.1	195	8	ADM98292	Adm98292	Outer mem	244	94	5.2	2399	6	ABU31130	ABu31130	Protein e


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RESULT 2
AAG67743
ID   AAG67743 standard; protein, 344 AA.
XX
XX
AC   AAG67743;
XX
XX   10-DEC-2001 (first entry)
XX
XX
DE   Amino acid sequence of a Klebsiella protein.
XX
XX   zwitterionic detergent; immune response; vaccine; IgA production;
XX   Igg response; tumour; viral infection; bacterial infection;
XX   parasitic infection.
XX
XX   Klebsiella pneumoniae.
XX
XX   FR2805163-A1.
XX
XX   24-AUG-2001.
XX
XX   21-FEB-2000; 2000FR-00002104.
XX
XX   21-FEB-2000; 2000FR-00002104.
XX
XX   (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
XX   Goestch L, Corvaia N, Beck A, Haeuw JF;
XX
XX   WPI; 2001-591759/67.
XX
XX   N-PSDB; AAH78461.
XX
XX   Mucosally administered vaccines containing zwitterionic detergents to
XX   induce or improve immune response towards antigen or hapten, especially
XX   used in antibacterial, antiviral, antiparasitic or antitumor vaccines.
XX
XX   Disclosure; Page 21-22; 26pp; French.
XX
XX
XX   The present sequence represents a Klebsiella protein. The protein is
XX   administered to test the adjuvant effect of zwitterionic detergents. The
XX   specification describes the use of zwitterionic detergents in the
XX   preparation of a mucosally administered pharmaceutical composition for
XX   inducing or improving the immune response of a mammal towards an antigen
XX   or hapten. In presence of zwitterionic detergents, vaccines are effective
XX   on mucosal (especially nasal) administration, which has the general
XX   advantages of inducing specific IgA production directly at the site of
XX   infection, stimulating a systemic IgG-type response (creating a secondary
XX   barrier against infection) and being simpler to carry out than
XX   administration by injection. The pharmaceutical composition is
XX   specifically a vaccine for the treatment or prophylaxis of tumours or
XX   viral, bacterial or parasitic infections
XX
XX   SQ   Sequence 344 AA;
XX
XX   Query Match      100.0%; Score 1822; DB 4; Length 344;
XX   Best Local Similarity 100.0%; Pred. No. 1.6e-157;
XX   Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX   Qy   1 MKALFVLNAAPKDNTWYAGKLGWSQYHDTGFGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
XX   Db   1 MKALFVLNAAPKDNTWYAGKLGWSQYHDTGFGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
XX
XX   Qy   61 PYLGFEMGYDNLGRMAYKGSVDNGAFKAQGVOLTAFLGYPTDLDLIYTRLGGMVWRADS 120
XX   Db   61 PYLGFEMGYDNLGRMAYKGSVDNGAFKAQGVOLTAFLGYPTDLDLIYTRLGGMVWRADS 120
XX
XX   Qy   121 KGNVASTGVSSEHDTGVSFVAGGVEWAVTRDIATRLLEYQVNNIGDAGTVGTRPDNGM 180
XX   Db   121 KGNVASTGVSSEHDTGVSFVAGGVEWAVTRDIATRLLEYQVNNIGDAGTVGTRPDNGM 180
XX
XX   Qy   181 LSLGVSRYFGQEDAAPVVPAPAPAPAPEVATKHFTLKSDVLFNFNFKATLKPEGQALDQLY 240
XX   Db   181 LSLGVSRYFGQEDAAPVVPAPAPAPAPEVATKHFTLKSDVLFNFNFKATLKPEGQALDQLY 240

241 TQLSNMDPKDGSVVVLGYTDRIIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGWGE 300
|||
241 TQLSNMDPKDGSVVVLGYTDRIIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGWGE 300
|||
301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPQA 344
|||
301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPQA 344
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RESULT 3
AAB84122
ID   AAB84122 standard; protein, 344 AA.
XX
XX   AAB84122;
XX
XX   06-AUG-2001 (first entry)
XX
XX   Amino acid sequence of a recombinant outer membrane protein A (rp40) .
XX
XX   Outer membrane protein A; rp40; OMP; enterobacterium; nasal vaccine;
XX   respiratory tract pathogen.
XX
XX   Klebsiella pneumoniae.
XX
XX   FR2801219-A1.
XX
XX   25-MAY-2001.
XX
XX   18-SEP-2000; 2000FR-00011862.
XX
XX   27-MAR-1998; 98FR-00003814.
XX
XX   (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
XX   Andreoni C, Raully I, Nguyen T, Haeuw JF, Baussant T;
XX
XX   WPI; 2001-358083/38.
XX
XX   N-PSDB; AAF90077.
XX
XX   Recombinant production of a protein, for particularly use as a carrier
XX   protein in nasal vaccines, comprises renaturation, after extraction, in
XX   the presence of specific detergents.
XX
XX   Claim 8; Page 26-27; 48pp; French.
XX
XX   The present sequence represents a recombinant outer membrane protein A,
XX   designated rp40. The specification describes a method for the recombinant
XX   production of a protein, or its fragments. The method comprises
XX   renaturation of the protein, after extraction, in the presence of a solution
XX   containing one of the detergents Zwittergent 3-14, Zwittergent 3-12 and
XX   octylglucopyranoside, where the protein is not beta-interferon. The
XX   protein is especially the outer membrane protein (OMP) from an
XX   enterobacterium, and is useful as a carrier for delivering antigens or
XX   haptens in a nasal vaccine formulation, particularly directed against
XX   pathogens of the respiratory tract, e.g. respiratory syncytial virus
XX   (RSV), (parainfluenza, hanta virus, Streptococci, Pneumococci and
XX   Meningococci, especially human or bovine RSV. Most adults show an
XX   antibody response to the Klebsiella pneumoniae p40, and this
XX   presensitisation stimulates the immune response to an antigen/hapten
XX   conjugated to the protein
XX
XX   SQ   Sequence 344 AA;
XX
XX   Query Match      100.0%; Score 1822; DB 4; Length 344;
XX   Best Local Similarity 100.0%; Pred. No. 1.6e-157;
XX   Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX   Qy   1 MKALFVLNAAPKDNTWYAGKLGWSQYHDTGFGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
XX   Db   1 MKALFVLNAAPKDNTWYAGKLGWSQYHDTGFGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
XX
XX   Qy   61 PYLGFEMGYDNLGRMAYKGSVDNGAFKAQGVOLTAFLGYPTDLDLIYTRLGGMVWRADS 120
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CC fragment of the gene for beta-hCG (human chorionic gonadotropin, beta-
CC chain), or one of its analogs, to prepare a pharmaceutical composition
CC for generating cytotoxic T lymphocytes (CTL). Peptides of the invention
CC associate with MHC Class I molecules to generate (I)-specific CTC,
CC causing expression of gamma-interferon and tumour necrosis factoralpha,
CC directed against HCG+ tumour cells. Peptides of the invention and nucleic
CC acids that encodes them, are used, particularly as vaccine, for treatment
CC or prevention of cancers that are positive for the HCG marker. The
CC current sequence represents the K. pneumoniae OmpA p40 amino acid
CC sequence.

Sequence 344 AA;

Query Match 99.5%; Score 1813; DB 8; Length 344;
Best Local Similarity 100.0%; Pred.No. 1.1e-156;
Matches 342; Conservative 0; Mismatches 0; Indels

[illegible]

RESULT 19
ABO60934
ID ABO60934 standard; protein: 385 AA.

AC ABO60934;

DT 29-JUL-2004 (first entry)

DE Klebsiella pneumoniae polypeptide seqid 7451.

KW Recombinant expression vector; transcription regulatory element;

[illegible]XX
клетка предназначена:[illegible]XX
DD XX-6007-07

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DR N-PSDB; ACH94485.

PT New nucleic acid

preparing a vaccine composition against *Klebsiella pneumoniae*.

Disclosure; SEQ ID NO 7451; 932pp; English.

The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against *Klebsiella pneumoniae*. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention

Sequence 385 AA;

every Match 97.7%; Score 1781; DB 7; Length 385;
 1st Local Similarity 99.1%; Pred. No. 1e-153;
 Hits 336; Conservative 0; Mismatches 3; Indels

6	VLNAAPKDNTWVAGCKLQWSQYHDTGFGYNGCFONNNGPTRNDOLCAGAEGGYQNPNPLGF	65
47	VAQAAPKDNTWVAGCKLQWSQYHDTGFGYNGCFONNNGPTRNDQLGAGAFGGYQNPNPLGF	106
66	EMGYDWLGMAKYKGSVDNGAFAKAQGVLTAKLGYPIITDDLDIYTRLGGVMWRADSKGNYA	125
107	EMGYDWLGMAKYKGSVDNGAFAKAQGVLTAKLGYPIITDDLDIYTRLGGVMWRADSKGNYA	166
126	STGVSRSEHDTCVSVPFAGGVGEAVTRDIATRELEYQWNNTGDAGTCTGTDPONGMLSLGV	185
167	STGVSRSEHDTCVSVPFAGGVGEAVTRDIATRELEYQWNNTIGDAGTVGTTRDPONGMLSLGV	226
186	SYRFGQEDAAPVPVAPAPAPAEVATKHFTLSKSDVLNFNKATLKPEGOALDQLYTQLSN	245
227	SYRFGQEDAAPVPVAPAPAPAEVATKHFTLSKSDVLNFNKATLKPEGOALDQLYTQLSN	286
246	MDPKDGSAVILGYTDRICSSEAYNQOLSEKRAQSVDVYLVAKGI PAKGISARGMGESNPVT	305
287	MDPKDGSAVILGYTDRICSSEAYNQOLSEKRAQSVDVYLVAKGI PAKGISARGMGESNPVT	346
306	GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTTQPOA	344
347	GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTTQPA A	385

RESULT 20

AAR88257

ID AAR88257 standard; protein; 335 AA.

AC AAR88257;

DT 15-MAY-1996 (first entry)

DE K.pneumoniae immunogenic adjuvant carrier protein p40.

Immunogenic peptide; protein G; respiratory syncytial virus; adjuvant; carrier protein; membrane lipopolysaccharide; LPS; *Klebsiella pneumoniae*; divalent cation; detergent; anion-exchange chromatography; infection.

OS *Klebsiella pneumoniae*.

PN FR2718452-A1.

PD 13-OCT-1995.

06-APR-1994; 94FR-00004009.

PR 06-APR-1994; 94FR-00004009.

PA (FABR) FABRE MEDICAMENT SA PIERRE.

PI Binz H, Thien NN, Baussant T, Trudel M;

DR WPI; 1995-353189/46.

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XX New respiratory syncytial virus polypeptide(s) for vaccine prodn. - esp.
PT by conjugation with new Klebsiella pneumoniae p40 protein.
XX
XX Disclosure; Page 27-29; 38pp; French.
XX
XX The amino acid sequence of the Klebsiella pneumoniae membrane
CC lipopolysaccharide (LPS) protein p40. The protein is used as an
CC immunogenic carrier protein for the peptides AAR8245-52 which are
CC derived from the protein G of the respiratory syncytial virus (RSV)
CC subgroups A and B. The p40 is isolated by precipitating the Klebsiella
CC membrane LPSs with a divalent cation and detergents, subjecting the
CC recovered proteins to anion-exchange chromatography to obtain the
CC immunological adjuvant and linking the p40 protein to the RSV peptides.
CC The conjugates are useful in the treatment of RSV A or B infections
XX
XX Sequence 335 AA;
SQ
    Query Match      97.2%; Score 1771; DB 2; Length 335;
    Best Local Similarity 100.0%; Pred. No. 7e-153;
    Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Qy 10 APKNTWTYAGKLGWSQYHDTGFYNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEY 69
    Db 1 APKNTWTYAGKLGWSQYHDTGFYNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEY 60
    Qy 70 DWLGRMAYKGSVDNGAFKAQGVLTAKLGYPTDLDLITRLGGMWRADSKGNYASTGV 129
    Db 61 DWLGRMAYKGSVDNGAFKAQGVLTAKLGYPTDLDLITRLGGMWRADSKGNYASTGV 120
    Qy 130 SRSEHDTGVSVPFAGGVEMAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGVSYRF 189
    Db 121 SRSEHDTGVSVPFAGGVEMAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGVSYRF 180
    Qy 190 QGEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 249
    Db 181 QGEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 240
    Qy 250 DGSAVVLGYTRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTC 309
    Db 241 DGSAVVLGYTRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTC 300
    Qy 310 DNVKARAALIDCLAPDRRVEIEVKYKEVVTQP 342
    Db 301 DNVKARAALIDCLAPDRRVEIEVKYKEVVTQP 333
RESULT 21
AAR95644
ID AAR95644 standard; protein; 335 AA.
XX
AC AAR95644;
XX
XX 14-JAN-1997 (first entry)
XX
DE Klebsiella pneumoniae P40 protein.
XX
XX Vaccine adjuvant; outer membrane protein OmpA; protein P40;
KW immune response; enhance.
XX
OS Klebsiella pneumoniae.
XX
XX Key Location/Qualifiers
FH 1..335
FT Protein /label= P40
FT Peptide 1..179
FT /note= "specifically claimed subfragment, i.e. P40
FT lacking immunogenic periplasmic C-terminal region"
FT 108..179
FT Peptide
FT /note= "specifically claimed subfragment, i.e. containing
FT the third and fourth extra-membrane loops flanking an
FT intra-membrane sequence"
FT 127..179
FT Peptide
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PT /note= "specifically claimed subfragment, i.e. containing
FT an invariant extra-membrane loop and the adjacent intra-
XX membrane sequence"
XX WO9614415-A1.
XX PN 17-MAY-1996.
XX PD
XX XX
XX PF 07-NOV-1995; 95WO-FR001463.
XX XX
XX PR 07-NOV-1994; 94FR-00013306.
XX XX
XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.
XX XX
XX FI Binz H, Baussant T, Haeuw J, Nguyen Ngoc T;
XX DR WPI; 1996-251765/25.
XX DR N-PSDB; AAT31607.
XX XX
XX PT Adjuvant protein derived from Klebsiella pneumoniae P40 protein -
FT enhances immunogenicity of antigen in immune complexes.
XX
XX Claim 6; Page 24-25; 46pp; French.
XX PS
XX CC The P40 protein from Klebsiella pneumoniae acts as an adjuvant for
XX enhancing the immunogenic activity of an antigen upon delivery to host.
XX Subfragments of P40 can also be used as adjuvants. Preferred P40-derived
XX fragments are: (1) a fragment lacking the immunogenic periplasmic C-
XX terminal region, (2) a fragment containing the third and fourth extra-
XX membrane loops flanking an intra-membrane sequence and (3) a fragment
XX containing an invariant extra-membrane loop and the adjacent intra-
XX membrane sequence
XX
XX SQ Sequence 335 AA;
    Query Match      97.2%; Score 1771; DB 2; Length 335;
    Best Local Similarity 100.0%; Pred. No. 7e-153;
    Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Qy 10 APKNTWTYAGKLGWSQYHDTGFYNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEY 69
    Db 1 APKNTWTYAGKLGWSQYHDTGFYNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEY 60
    Qy 70 DWLGRMAYKGSVDNGAFKAQGVLTAKLGYPTDLDLITRLGGMWRADSKGNYASTGV 129
    Db 61 DWLGRMAYKGSVDNGAFKAQGVLTAKLGYPTDLDLITRLGGMWRADSKGNYASTGV 120
    Qy 130 SRSEHDTGVSVPFAGGVEMAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGVSYRF 189
    Db 121 SRSEHDTGVSVPFAGGVEMAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGVSYRF 180
    Qy 190 QGEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 249
    Db 181 QGEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 240
    Qy 250 DGSAVVLGYTRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTC 309
    Db 241 DGSAVVLGYTRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTC 300
    Qy 310 DNVKARAALIDCLAPDRRVEIEVKYKEVVTQP 342
    Db 301 DNVKARAALIDCLAPDRRVEIEVKYKEVVTQP 333
RESULT 22
AAR93796
ID AAR93796 standard; protein; 335 AA.
XX
XX AAR93796;
AC AAR93796;
XX
XX 16-SEP-1998 (first entry)
DT
XX Protein P40, and OMPA protein from K. pneumoniae I-145.
DE
```

XX Outer membrane protein; OmpA; P40; immunocomplex; oligosaccharide;
KW polysaccharide; vaccine; Salmonella.
OS Klebsiella pneumoniae.
XX WO9741888-A1.
XX 13-NOV-1997.
PD 06-MAY-1997; 97WO-FR000800.
PF 07-MAY-1996; 96FR-00005692.
PR (FABR) FABRE MEDICAMENT SA PIERRE.
XX Binz H, Haeuw J, Svenson S;
DR WPI; 1997-558694/51.
DR N-PSDB; AAV13867.
XX Immunogenic complex for use in anti-bacterial vaccine - comprises
PT bacterial oligo; or poly:saccharide coupled to a Gram-negative bacterial
PT outer membrane protein or a Streptococcal HSA binding protein.
XX Claim 11,12,20; Page 35-36; 63pp; French.
XX The patent discloses a new immunogenic complex which consists of (1) an
CC oligo- or polysaccharide found naturally on bacteria, coupled to (2) a
CC carrier protein chosen from (a) the human serum albumin binding protein
CC of Streptococcus, (b) Gram-negative bacterial outer membrane proteins
CC (Omp), or (c) fragments of these proteins. The immunogenic complex is
CC useful in a vaccine to protect animals against infection by Salmonella,
CC especially those belonging to antigenic specificity group O:9, including
CC S. enteritidis, S. panama and S. dublin. A vaccine prepared using an
CC oligosaccharide from S. enteritidis can be used to provide protection
CC against septicaemia caused by S. typhi and against typhoid fever, as well
CC as to protect humans and animals from toxic infections and zoonosis
CC caused by Salmonella of the same serogroup. The carrier proteins enhance
CC the immunogenicity of the oligo- or polysaccharide antigens. Inclusion of
CC additional Salmonella capsule antigens, such as the Vi antigen, increases
CC the vaccine's efficacy against encapsulated bacteria. The present
CC sequence, protein P40 from Kleb. pneumoniae i-145, is a preferred example
CC of a carrier protein which can be used in the immunocomplex
XX Sequence 335 AA;
Query Match 97.2%; Score 1771; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 7e-153;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 APKDNWTWAGGKLGWSQVHDTGFGNGFQNNNGPTRNDOLGAGAFGGVQVNPYLGFMGY 69
Db 1 APKDNWTWAGGKLGWSQVHDTGFGNGFQNNNGPTRNDOLGAGAFGGVQVNPYLGFMGY 60
Qy 70 DWLGRMAYKGSVDNGAFKAGQVQLTAKLGYPITDLDIYTRLGGMVWRADSKGNVYSTGV 129
Db 61 DWLGRMAYKGSVDNGAFKAGQVQLTAKLGYPITDLDIYTRLGGMVWRADSKGNVYSTGV 120
Qy 130 SRSEHDTGVSVPFAGGVEMWATRIATRLFYQVNNIGDAGTVGTRPDNGMLSGVSYRF 189
Db 121 SRSEHDTGVSVPFAGGVEMWATRIATRLFYQVNNIGDAGTVGTRPDNGMLSGVSYRF 180
Qy 190 GQEDAAPVWAPAPAPAPVATKFTLSDVLFNFNKATLKEGQOALDQLYTQLSNMDDPK 249
Db 181 GQEDAAPVWAPAPAPAPVATKFTLSDVLFNFNKATLKEGQOALDQLYTQLSNMDDPK 240
Qy 250 DGSVAVLGTYDRIIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPTVNTC 309
Db 241 DGSVAVLGTYDRIIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPTVNTC 300
Qy 310 DNVKARAALIDCLAPDRRVEIEVKYKEVVTQP 342

Db 301 DNVKARAALIDCLAPDRRVEIEVKYKEVVTQP 333
RESULT 23
ABM69278
ID ABM69278 standard; protein; 369 AA.
XX ABM69278;
AC ABM69278;
DT 20-NOV-2003 (first entry)
XX Photorhabdus luminescens protein sequence #2375.
DE Photorhabdus luminescens.
XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough.
XX Photorhabdus luminescens.
OS W0200294867-A2.
XX 28-NOV-2002.
PD 07-FEB-2002; 2002WO-IB003040.
PF 07-FEB-2001; 2001FR-00001659.
PR (INSP) INST PASTEUR.
XX (CNRS) CNRS CENT NAT RECH SCI.
PA Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX WPI; 2003-148459/14.
DR Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
XX useful e.g. as therapeutic antimicrobials and agricultural pesticides.
PT Claim 2; SEQ ID NO 2375; 1205pp; French.
XX The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens proteins
XX Sequence 369 AA;
Query Match 71.0%; Score 1294; DB 6; Length 369;
Best Local Similarity 70.1%; Pred. No. 2.9e-109;
Matches 242; Conservative 38; Mismatches 55; Indels 10; Gaps 3;
Qy 9 AAPKDNWTWAGGKLGWSQVHDTGFGNGFQNNNGPTRNDOLGAGAFGGVQVNPYLGFE 66
Db 21 AAPKDNWTWAGGKLGWSQVHDTGFGNGFQNNNGPTRNDOLGAGAFGGVQVNPYLGFE 80

CC S. enteritidis, S. panama and S. dublin. A vaccine prepared using an
 CC oligosaccharide from S. enteritidis can be used to provide protection
 CC against septicaemia caused by S. typhi and against typhoid fever, as well
 CC as to protect humans and animals from toxic infections and zoonosis
 CC caused by Salmonella of the same serogroup. The carrier proteins enhance
 CC the immunogenicity of the oligo- or polysaccharide antigens. Inclusion of
 CC additional Salmonella capsule antigens, such as the Vi antigen, increases
 CC the vaccine's efficacy against encapsulated bacteria. The present
 CC sequence, L-Delta-P40-F8, is a preferred example of a carrier protein
 CC which can be used in the immunocomplex. It is obtained by recombinant
 CC expression of a modified kleb. pneumoniae I-145 P40 gene in E. coli
 XX
 SQ Sequence 188 AA;

Query Match 56.3%; Score 1026; DB 2; Length 188;
 Best Local Similarity 100.0%; Pred. No. 3.4e-85;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAIFVLNAAPKDNVTWAGGKLGHSQYHDTGFGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
 Db 1 MKAIFVLNAAPKDNVTWAGGKLGHSQYHDTGFGNGFQNNNGPTRNDQLGAGAFGGYQVN 60

Qy 61 PYLGFEMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPIITDDLDIYTRLGGMWRADS 120
 Db 61 PYLGFEMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPIITDDLDIYTRLGGMWRADS 120

Qy 121 KGNVASTGVSRSRSHDGTGSPVFAGGVEWAVTRDIATRLQYQWVNNIGDAGTGTGTRPDNGM 180
 Db 121 KGNVASTGVSRSRSHDGTGSPVFAGGVEWAVTRDIATRLQYQWVNNIGDAGTGTGTRPDNGM 180

Qy 181 LSLGVSYR 188
 Db 181 LSLGVSYR 188

RESULT 26
 AAR95645
 ID AAR95645 standard; protein; 179 AA.
 XX
 AC AAR95645;
 XX
 DT 14-JAN-1997 (first entry)
 XX
 DE Klebsiella pneumoniae P40 protein fragment, amino acids 1-179.
 XX
 KW Vaccine adjuvant; outer membrane protein OmpA; protein P40;
 KW immune response; enhance.
 XX
 OS Klebsiella pneumoniae.
 XX
 PN WO9614415-A1.
 XX
 PD 17-MAY-1996.
 XX
 PF 07-NOV-1995; 95WO-FR001463.
 XX
 PR 07-NOV-1994; 94FR-00013306.
 XX
 PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX
 PI Binz H, Baussant T, Haeuw J, Nguyen Ngoc T;
 XX
 DR WPI; 1996-251765/25.
 DR N-PSDB; AAT31608.
 XX
 FT Adjuvant protein derived from Klebsiella pneumoniae P40 protein -
 PT enhances immunogenicity of antigen in immune complexes.
 XX
 PS Claim 6; Page 26-27; 46pp; French.
 XX
 CC The P40 protein from Klebsiella pneumoniae acts as an adjuvant for
 CC enhancing the immunogenic activity of an antigen upon delivery to host.
 CC Subfragments of P40 can also be used as adjuvants. Preferred P40-derived

CC fragments are: (1) a fragment lacking the immunogenic periplasmic C-
 CC terminal region, (2) a fragment containing the third and fourth extra-
 CC membrane loops flanking an intra-membrane sequence and (3) a fragment
 CC containing an invariant extra-membrane loop and the adjacent intra-
 CC membrane sequence. The present sequence corresponds to amino acids 1-179
 CC of P40 (i.e. fragment (1))
 XX
 SQ Sequence 179 AA;

Query Match 54.0%; Score 984; DB 2; Length 179;
 Best Local Similarity 100.0%; Pred. No. 2.2e-81;
 Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 APKDNVTWAGGKLGWSQYHDTGFGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFMGY 69
 Db 1 APKDNVTWAGGKLGWSQYHDTGFGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFMGY 60

Qy 70 DWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPIITDDLDIYTRLGGMWRADSKGNYASTGV 129
 Db 61 DWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPIITDDLDIYTRLGGMWRADSKGNYASTGV 120

Qy 130 SRSEHDTGVSFVAGGVEWAVTRDIATRLQYQWVNNIGDAGTGTGTRPDNGMLSLGVSYR 188
 Db 121 SRSEHDTGVSFVAGGVEWAVTRDIATRLQYQWVNNIGDAGTGTGTRPDNGMLSLGVSYR 179

RESULT 27
 ABB83156
 ID ABB83156 standard; protein; 137 AA.
 XX
 AC ABB83156;
 XX
 DT 09-AUG-2002 (first entry)
 XX
 DE Partial OmpA protein sequence, P40.
 XX
 KW OmpA; outer membrane protein; enterobacterium; infection; tumour; P40;
 KW virucide; antibacterial; antiparasitic; fungicide; cytostatic; vaccine.
 XX
 OS Klebsiella pneumoniae.
 XX
 PN WO200240518-A1.
 XX
 PD 23-MAY-2002.
 XX
 PF 16-NOV-2001; 2001WO-FR003596.
 XX
 PR 17-NOV-2000; 2000FR-00014909.
 XX
 PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX
 PI Goetsch L, Haeuw J, Robert A;
 XX
 DR WPI; 2002-454861/48.
 DR N-PSDB; ABB83312.
 XX
 PT Composition containing enterobacterial outer membrane peptides, useful
 PT e.g. as vaccine carrier or adjuvant, derived from the protein's
 PT periplasmic domain.
 XX
 PS Claim 4; Page 23; 30pp; French.
 XX
 CC The present invention relates to pharmaceutical compositions, which
 CC comprise at least one peptide (I) from the periplasmic domain of an outer
 CC membrane protein (Omp) of an enterobacteria or a nucleic acid construct
 CC that encodes (I). The present sequence corresponds to residues 199 to 335
 CC of the OmpA protein of Klebsiella pneumoniae (P40). The compositions are
 CC useful (i) as carriers and adjuvants in vaccines for treatment or
 CC prevention of infections (viral, bacterial, parasitic or fungal,
 CC particularly respiratory syncytial virus) or tumours; or (ii) to
 CC generate, or improve, the immune response against infectious agents or
 CC tumour cells
 XX

XX AC AAM50719; /label= Mature_protein

XX PN WO200204485-A1.

XX DT 17-JAN-2002.

XX DE 06-JUL-2001; 2001WO-AU000822.

XX PF 07-JUL-2000; 2000AU-00008652.

XX PR (UYQU) UNIV QUEENSLAND.

XX PA Terry TD, Tseng H, Hobb RI, Jennings MP, Downes J;

XX PI WPI; 2002-154917/20.

XX DR N-PSDB; ABA91419.

XX DX New haemagglutinin polypeptide isolated from Haemophilus paragallinarum useful as a vaccine for immunizing chickens against coryza caused by the species.

XX PT Claim 2; Fig 4; 67pp; English.

XX PS The present sequence is that of the HagA haemagglutinin of Haemophilus paragallinarum strain 2403 (serovar A), the causative agent of infectious coryza in chickens. The invention provides recombinant haemagglutinin polypeptides (see AAM50716-27) and encoding nucleic acids (see ABA91417-27) from 11 strains (serovars A, B and C) of H. paragallinarum, the causative agent of infectious coryza of chickens. The polypeptides are useful in vaccines for immunisation against infectious coryza, as are the nucleic acids when expressed in attenuated bacteria, especially Salmonella or Mycoplasma (claimed). The recombinant polypeptide is preferably the mature protein, or a biologically active fragment, variant or derivative, that is capable of eliciting an immune response, providing protection against one or more strains of H. paragallinarum in chickens. Also claimed are methods of using the haemagglutinin polypeptides and nucleic acids for detection and diagnosis of infectious coryza in chickens

XX SQ Sequence 344 AA;

Query Match 37.6%; Score 685; DB 5; Length 344;

Best Local Similarity 44.9%; Pred. No. 1.1e-53;

Matches 153; Conservative 46; Mismatches 124; Indels 18; Gaps 7;

QY 1 MKAIFVLNAPKNDNTWYAGKLGWSQYHDTGFGYNGFQNNNGPTENDOLGAGAFGGYQVN 60

DB 13 LTAASVAQAAPQANTFYAGAKAGWASFDGLNQLQFNSQNAQDGLTRN-SVTYGVFGGYQIT 71

QY 61 PYLGFEMGVDMGLGRMAYKGSVDN-GAFKAQGVQLTAKLGYPTDLDLIYTLGLGMVWRAD 119

DB 72 DNFAVELGYDDFGRAKLRQDGETVKGKTHNHGAHLSLKASYPVLEGLDYARVGAALTRSD 131

QY 120 SKGNVASTGVSRSSEHDTGVSVPFAGGVEWAVTR--DIATRLLEYQWVNNIG----DAGTVG 173

DB 132 YKPTKRAAPNQTTHSHSLKVSVPFAGGLEYNLPSLPALRLVEYQWNVKGVREKDGSRVD 191

QY 174 TRPDNGMLSLGVSYRFGQEDAAPVVPAPAPAPAVEATVKHFTLKSDVLFNFNKATLKPEQG 233

DB 192 YTPSIGSVTAGLSYRFGQ--SAPVW-----EPKVVAKTFALNSDVTFAFKANLRPEAQ 243

QY 234 QALDOLYLTOLSNMDPKDGSVVLGYTDRIGSAYNQOLSEKRAQSVVDYLVAKGIPAGKI 293

DB 244 NVLDGIYGEIAQI--KSVQVDVAGYTDRIGSBAANLKLQSRRADTVANILVSKGVAQEV 301

QY 294 SARGMGESNPVTGNTCDNKARAALIDCLAPDRRVEIEVK 334

DB 302 SSTGYGEANPVTGAKCDTVKGRKALIACLADDRRVEISVK 342

RESULT 32

AAM50719

ID AAM50719 standard; protein; 344 AA.

Db	192	YTPSIGSVTAGLSYRFGQ--SAPVV-----EPKVAKTFALNSDVTFAFGKANLRPEAQ	243
Qy	234	QALDQLYTQLSNMOPKDGSAVVLGYTDRIGSEAYNQSLSEKRAOSVVDYLVAKGIPAGKI	293
Db	244	NVLDDIYGEIAQL--KSVQVDLAGYTDRIIGSEANLKSQRADTVANLYLSKGVQAEVI	301
Qy	294	SARGMGSNPVTGNTCDNVKARAALIDCLAPDRRVEIVKG	334
Db	302	SSTGYGEANPVTGAKCDVAKGRKALIACLADRRRVEISVKG	342
RESULT 33			
ID	AAM50717	standard; protein; 344 AA.	
AC	AAM50717;		
XX	18-APR-2002	(first entry)	
DT	Haemophilus	paragallinarum strain 221 haemagglutinin.	
DE	Haemagglutinin;	HagA; antigen; vaccine; immunisation; coryza; chicken.	
KW	Haemophilus	paragallinarum.	
OS	Haemophilus	paragallinarum.	
XX	Key	Location/Qualifiers	
FH	Peptide	1..21	
FT	Protein	/label= Signal_peptide	
FT		22..344	
FT		/label= Mature_protein	
XX	WO200204485-A1.		
PN	17-JAN-2002.		
XX	06-JUL-2001;	2001WO-AU000822.	
XX	07-JUL-2000;	2000AU-00008652.	
XX	(UYQU)	UNIV QUEENSLAND.	
XX	Terry TD,	Tseng H, Hobb RI, Jennings MP, Downes J;	
PI	WPI;	2002-154917/20.	
DR	N-PSDB;	ABA91418.	
XX	New haemagglutinin polypeptide isolated from Haemophilus paragallinarum		
PT	useful as a vaccine for immunizing chickens against coryza caused by the		
PT	species.		
XX	Claim 2;	Fig 4; 67pp; English.	
PS	The present sequence is that of the HagA haemagglutinin of Haemophilus		
CC	paragallinarum strain 221 (serovar A), the causative agent of infectious		
CC	coryza in chickens. The invention provides recombinant haemagglutinin		
CC	polypeptides (see AAM50716-27) and encoding nucleic acids (see ABA91417-		
CC	27) from 11 strains (serovars A, B and C) of H. paragallinarum, the		
CC	causative agent of infectious coryza of chickens. The polypeptides are		
CC	useful in vaccines for immunisation against infectious coryza, as are the		
CC	nucleic acids when expressed in attenuated bacteria, especially		
CC	Salmonella or Mycoplasma (claimed). The recombinant polypeptide is		
CC	preferably the mature protein, or a biologically active fragment, variant		
CC	or derivative, that is capable of eliciting an immune response, providing		
CC	protection against one or more strains of H. paragallinarum in chickens.		
CC	Also claimed are methods of using the haemagglutinin polypeptides and		
CC	nucleic acids for detection and diagnosis of infectious coryza in		
CC	chickens		
XX	Sequence 344 AA;		
SQ	Query Match	37.5%; Score 684; DB 5; Length 344;	
	Best Local Similarity	44.6%; Pred. NO. 1.4e-53;	

Matches 152;	Conservative 46;	Mismatches 125;	Indels 18;	Gaps 7;
Qy	1	MKAIFLVNAAPKONTYAGKLGWSQYHDTGFCFYGNQNNNGPTRNDQLGAGAFGGYQVN	60	
Db	13	LTAASVAQAAPQANTTFAGAKAGWASHFDGLNQFPENSONAYGTLRN-SVTYGVFGYQIT	71	
Qy	61	PYLGFGNGYDNLGRMAYKGSVDN-GAPKAQGVQLTAKGYPTITDDLDIYTRLGGMWRAD	119	
Db	72	DNFAVELGYDDPFGRAKLQDGETVGKHTNHGAHLKSASYPVLSEGLDVYARVGAALIRSD	131	
Qy	120	SKGNYASTGVSRSEHDTGVSFAGGVGEWAVTR--DIATBLEYQMVNIG---DAGTVG	173	
Db	132	YKPTKRAAPNETHEHSLSKSPVFAGGLEYNLPSLPELALRVEYQMVNKGWEXDGSRVD	191	
Qy	174	TRPDNGMLSLGVSYRFQGEDAAPVWAPAPAPAPAVATKHFCLKSDVLFNFKATLKPEGQ	233	
Db	192	YTPSIGSVTAGLSYRFGQ--SAPVV-----EPKVAKTFALNSDVTFAFGKANLRPEAQ	243	
Qy	234	QALDQLYTQLSNMOPKDGSAVVLGYTDRIGSEAYNQSLSEKRAOSVVDYLVAKGIPAGKI	293	
Db	244	NVLDDIYGEIAQL--KSVQVDLAGYTDRIIGSEANLKSQRADTVANLYLSKGVQAEVI	301	
Qy	294	SARGMGSNPVTGNTCDNVKARAALIDCLAPDRRVEIVKG	334	
Db	302	SSTGYGEANPVTGAKCDVAKGRKALIACLADRRRVEISVKG	342	
RESULT 34				
ID	AAM50716	standard; protein; 344 AA.		
XX	AAM50716;			
XX	18-APR-2002	(first entry)		
DT	Haemophilus	paragallinarum strain 0083 haemagglutinin.		
DE	Haemagglutinin;	HagA; antigen; vaccine; immunisation; coryza; chicken.		
KW	Haemophilus	paragallinarum.		
OS	Haemophilus	paragallinarum.		
XX	Key	Location/Qualifiers		
FH	Peptide	1..21		
FT	Protein	/label= Signal_peptide		
FT		22..344		
FT		/label= Mature_protein		
XX	WO200204485-A1.			
PN	17-JAN-2002.			
XX	06-JUL-2001;	2001WO-AU000822.		
XX	07-JUL-2000;	2000AU-00008652.		
XX	(UYQU)	UNIV QUEENSLAND.		
XX	Terry TD,	Tseng H, Hobb RI, Jennings MP, Downes J;		
PI	WPI;	2002-154917/20.		
DR	N-PSDB;	ABA91417.		
XX	New haemagglutinin polypeptide isolated from Haemophilus paragallinarum			
PT	useful as a vaccine for immunizing chickens against coryza caused by the			
PT	species.			
XX	Claim 2;	Fig 4; 67pp; English.		
PS	The present sequence is that of the HagA haemagglutinin of Haemophilus			
CC	paragallinarum strain 0083 (serovar A), the causative agent of infectious			
CC	coryza in chickens. The invention provides recombinant haemagglutinin			
CC	polypeptides (see AAM50716-27) and encoding nucleic acids (see ABA91417-			
CC	27) from 11 strains (serovars A, B and C) of H. paragallinarum, the			
CC	causative agent of infectious coryza of chickens. The polypeptides are			
CC	useful in vaccines for immunisation against infectious coryza, as are the			
CC	nucleic acids when expressed in attenuated bacteria, especially			
CC	Salmonella or Mycoplasma (claimed). The recombinant polypeptide is			
CC	preferably the mature protein, or a biologically active fragment, variant			
CC	or derivative, that is capable of eliciting an immune response, providing			
CC	protection against one or more strains of H. paragallinarum in chickens.			
CC	Also claimed are methods of using the haemagglutinin polypeptides and			
CC	nucleic acids for detection and diagnosis of infectious coryza in			
CC	chickens			
XX	Sequence 344 AA;			
SQ	Query Match	37.5%; Score 684; DB 5; Length 344;		
	Best Local Similarity	44.6%; Pred. NO. 1.4e-53;		


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FT      Protein      /label= Signal_peptide
FT      22..344
FT      /label= Mature_protein
FN      WO200204485-A1.
PN      17-JAN-2002.
XX      06-JUL-2001; 2001WO-AU000822.
XX      07-JUL-2000; 2000AU-00008652.
XX      (UYQU ) UNIV QUEENSLAND.
XX      Terry TD, Tseng H, Hobb RI, Jennings MP, Downes J;
XX      WPI; 2002-154917/20.
XX      N-PSDB; ABA91426.
XX      New haemagglutinin polypeptide isolated from Haemophilus paragallinarum
XX      useful as a vaccine for immunizing chickens against coryza caused by the
XX      species.
XX      Claim 2; Fig 4; 67pp; English.
XX      The present sequence is that of the HagA haemagglutinin of Haemophilus
XX      paragallinarum strain SA-3 (serovar C), the causative agent of infectious
XX      coryza in chickens. The invention provides recombinant haemagglutinin
XX      polypeptides (see AAM50716-27) and encoding nucleic acids (see ABA91417-
XX      27) from 11 strains (serovars A, B and C) of H. paragallinarum, the
XX      causative agent of infectious coryza of chickens. The polypeptides are
XX      useful in vaccines for immunisation against infectious coryza, as are the
XX      nucleic acids when expressed in attenuated bacteria, especially
XX      Salmonella or Mycoplasma (claimed). The recombinant polypeptide is
XX      preferably the mature protein, or a biologically active fragment, variant
XX      or derivative, that is capable of eliciting an immune response, providing
XX      protection against one or more strains of H. paragallinarum in chickens.
XX      Also claimed are methods of using the haemagglutinin polypeptides and
XX      nucleic acids for detection and diagnosis of infectious coryza in
XX      chickens
XX      SQ      Sequence 344 AA;
XX      Query Match      37.5%; Score 683; DB 5; Length 344;
XX      Best Local Similarity 44.6%; Pred. No. 1.7e-53;
XX      Matches 152; Conservative 46; Mismatches 125; Indels 18; Gaps 7;
Qy      1 MKAIFVLNAAPKDNTWYAGKLGHSQVHDTGFGYNGFQNNNGPTRNDQLGAGAFGGYQVN 60
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      13 LTAASVAQAAPQANTFYAGAKAGWASFHDLGNQFENSQNAVYGTLLRN-SVTYGVFGGYQIT 71
Qy      61 PYLGFEMGYDVLGRMAYKGSVDN-GAFKAQGVOLTAKLGYPIITDDLDIYTRLGGMWVRAD 119
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      72 DNFAVELGYDDFGRAKLQDGETVGKHTNTHGAHLSLKASYPVLEGLDVIYARVGAALIRSD 131
Qy      120 SKGNYASTGVSRSSEHDTGVSFVAGGVEWAVTR--DIATRLLEYQWVNNIG----DAGTVG 173
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      132 YKPTKRAAPNETHEHTLKVSPFVAGGLEYNLPSLPALALRVEYQWVNVKGRWEXDGSRDV 191
Qy      174 TRPONGMLSLGVSRYRFGGEDAAPVAPAPAPAEVATKHFTLKSDVLNFNFNKAATLKPEQG 233
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      192 YTPSTGVSVTAGLSYRFGQ--SAPVV-----EPKVAKTFALNSDVTFAFGKANLRPEAQ 243
Qy      234 QALDOLYTLQSLNMPDKGSADVVLGYDTRIGSEAYNQOLSEKRAOSVVDYLVAKGIPAGKI 293
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      244 NVLDGIYGEIAQL--KSVQVDLAGYTDRIKGEAANLKLSQRRADTVANILVSKGVAQEV 301
Qy      294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      302 SSTGGEANPYTGAKCDVAKGRKALLACLAADRRRVEISVKG 342
XX      RESULT 37

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AAM50720
ID      AAM50720 standard; protein; 341 AA.
XX      AC      AAM50720;
XX      DT      18-APR-2002 (first entry)
XX      DE      Haemophilus paragallinarum strain HP14 haemagglutinin.
XX      KW      Haemagglutinin; HagA; antigen; vaccine; immunisation; coryza; chicken.
XX      OS      Haemophilus paragallinarum.
XX      FH      Key      Location/Qualifiers
XX      FT      Peptide      1..21
XX      FT      Protein      22..341
XX      FT      /label= Signal_peptide
XX      FT      /label= Mature_protein
XX      FN      WO200204485-A1.
XX      PD      17-JAN-2002.
XX      PF      06-JUL-2001; 2001WO-AU000822.
XX      PR      07-JUL-2000; 2000AU-00008652.
XX      PA      (UYQU ) UNIV QUEENSLAND.
XX      PI      Terry TD, Tseng H, Hobb RI, Jennings MP, Downes J;
XX      DR      WPI; 2002-154917/20.
XX      DR      N-PSDB; ABA91421.
XX      PT      New haemagglutinin polypeptide isolated from Haemophilus paragallinarum
XX      useful as a vaccine for immunizing chickens against coryza caused by the
XX      species.
XX      Claim 2; Fig 4; 67pp; English.
XX      The present sequence is that of the HagA haemagglutinin of Haemophilus
XX      paragallinarum strain HP14 (serovar A), the causative agent of infectious
XX      coryza in chickens. The invention provides recombinant haemagglutinin
XX      polypeptides (see AAM50716-27) and encoding nucleic acids (see ABA91417-
XX      27) from 11 strains (serovars A, B and C) of H. paragallinarum, the
XX      causative agent of infectious coryza of chickens. The polypeptides are
XX      useful in vaccines for immunisation against infectious coryza, as are the
XX      nucleic acids when expressed in attenuated bacteria, especially
XX      Salmonella or Mycoplasma (claimed). The recombinant polypeptide is
XX      preferably the mature protein, or a biologically active fragment, variant
XX      or derivative, that is capable of eliciting an immune response, providing
XX      protection against one or more strains of H. paragallinarum in chickens.
XX      Also claimed are methods of using the haemagglutinin polypeptides and
XX      nucleic acids for detection and diagnosis of infectious coryza in
XX      chickens
XX      SQ      Sequence 341 AA;
XX      Query Match      37.3%; Score 680.5; DB 5; Length 341;
XX      Best Local Similarity 44.7%; Pred. No. 2.8e-53;
XX      Matches 151; Conservative 47; Mismatches 125; Indels 15; Gaps 7;
Qy      1 MKAIFVLNAAPKDNTWYAGKLGHSQVHDTGFGYNGFQNNNGPTRNDQLGAGAFGGYQVN 60
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      13 LTAASVAQAAPQANTFYAGAKAGWASFHDLGNQFENSQNAVYGTLLRN-SVTYGVFGGYQIT 71
Qy      61 PYLGFEMGYDVLGRMAYKGSVDN-GAFKAQGVOLTAKLGYPIITDDLDIYTRLGGMWVRAD 119
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      72 DNFAVELGYDDFGRAKLQDGETVGKHTNTHGAHLSLKASYPVLEGLDVIYARVGAALIRSD 131
Qy      120 SKGNYASTGVSRSSEHDTGVSFVAGGVEWAVTR--DIATRLLEYQWVNNIG--DAGTVGTRP 176
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      132 YKPTKRAAPNETHEHTLKVSPFVAGGLEYNLPSLPALALRVEYQWVNVKGRDGSRDV 191

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Db 192 YTPSIGSVTGLSYRFGQ--SAPVV-----EPKVAKTFALNSDVTFAFGKANLRPEAQ 243
Qy 234 QALDQLYTQLSNMPPKDGSAVVLGYTDRIGSEAYNQSLSEKRAQSVVDYLVAKGIPAGKI 293
Db 244 NVLDGIYGEIAQL--KSVQVDXAGYTDRIQSEAAANLKLSSRRADTVANLYLVSKGVAQEV 301
Qy 294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
Db 302 SSTGYGEANPVTGAKCDXVKGRKALIACLADRRRVEISVGK 342

RESULT 41
AAB44588
ID AAB44588 standard; protein; 364 AA.
XX
AC AAB44588;
XX
DT 08-FEB-2001 (first entry)
XX
DE Virulence gene protein #68.
XX
KW Virulence gene; antibacterial; vaccine; bacterial infection; septicemia;
KW bronchopneumonia; rhinitis; wound infection.
XX
OS Actinobacillus pleuropneumoniae.
XX
PN WO200061724-A2.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009218.
XX
PR 09-APR-1999; 99US-0128689P.
PR 10-SEP-1999; 99US-0153453P.
XX
PA (PHAA ) PHARMACIA & UPJOHN INC.
XX
PI Lowery DE, Fuller TE, Kennedy MJ;
XX
WPI; 2000-647422/62.
DR N-PSDB; AAC79663.
XX
PT Attenuated Pasteurellaceae bacteria comprising mutations in virulence
PT genes, useful as a live attenuated vaccine against bacterial infections.
XX
PS Claim 39; Page 305-306; 322pp; English.
XX
The family Pasteurellaceae encompasses several pathogens that infect a
CC wide variety of animals. The present invention relates to virulence genes
CC from Pasteurellaceae. The present sequence is a protein encoded by one
CC such virulence gene. The virulence genes of the present invention may be
CC mutated in order to produce an inactive gene. The inactive virulence gene
CC may in turn be used to produce a vaccine, which is useful for treating
CC bacterial infections such as septicemias, bronchopneumonias, rhinitis and
CC wound infections
XX
SQ Sequence 364 AA;

Query Match 36.8%; Score 671; DB 3; Length 364;
Best Local Similarity 42.4%; Pred. No. 2.3e-52;
Matches 153; Conservative 54; Mismatches 122; Indels 32; Gaps 10;

Qy 1 MKAIFVLNAAPKONTWYAGKLGWSQYHDTGFGYNGFQNNNGPTR----NDQLGAGAFGG 56
Db 11 LSAAVAQAAPQONTFYAGAKGAWSPFDGIEQLDSAKNTRDGTGKYGNRNSVTYGVFGG 70

Qy 57 YQV--NPYLGF--EMGYDWLGRM-----AYKGSVDNGAFK--AQGVQLTAKLGYPTDLDL 106
Db 71 YQILNQDKLGLAAELGYDYFGRVGRSEKPNKADKKTFRHAAGATIALKPSYEVLPDL 130

Qy 107 IYTRLG-GMWWRADSKGNVASTGVSRSEHDTGVPVFAGGVWEAVTRDIATRLYQWVNN 165
Db 131 VYGVKGIALVNNYKTFENAAQEKVKTRRFQS--SLILGAGVEYAILPELAARVEYQWLNN 188
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Qy 166 IGDA-----GTVGTRPDNGMLSLGVSYRFGEDAAPVVPAPAPAPAPVATKHFTLKS 217
Db 189 AGKASVSTLNRMGATDYRSISSVSAGLSYRFGQ-GAAPVAAPA-----VETKNFAFSS 241
Qy 218 DVLFFNFNKATLKPEGGQALDQLYTQLSNMPPKDGSAVVLGYTDRIGSEAYNQSLSEKRAQ 277
Db 242 DVLFAFGKSNLKPAAATALDAMQTEINNAGLSNAAIQVNGYTDRIQKEASNLKLSQRRAE 301
Qy 278 SVVDYLVAKGIPAGKISARGGSESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 337
Db 302 TVANYIVSKGAPAAVNTAVGYGEANPVTGATCDKVKGRKALIACLAPDRRVEVQVQGTKE 361

338 V 338
362 V 362

RESULT 42
ABP54540
ID ABP54540 standard; protein; 364 AA.
XX
AC ABP54540;
XX
DT 24-JAN-2003 (first entry)
XX
DE Actinobacillus pleuropneumoniae Omp5-2 protein SEQ ID NO:151.
XX
KW Antibacterial; vaccine; gram negative bacterial virulence gene;
KW identification; virulence; Pasteurellaceae.
XX
OS Actinobacillus pleuropneumoniae.
XX
PN WO200075507-A2.
XX
PD 26-SEP-2002.
XX
PF 17-JAN-2002; 2002WO-US001971.
XX
PR 15-MAR-2001; 2001US-00809665.
XX
PA (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI Lowery DE, Fuller TE, Kennedy MJ;
XX
WPI; 2002-740868/80.
DR N-PSDB; ABQ83540.
XX
New mutant gram-negative bacteria, useful as vaccines and for identifying
XX new anti-bacterial agents that target virulence genes and their products.
XX
Claim 36; Page 311-312; 350pp; English.
XX
The present invention describes a gram-negative bacteria comprising a
CC mutation in a gene, where the mutation results in decreased activity of a
CC gene product encoded by the mutated gene. Also described is a method for
CC producing a gram-negative bacteria mutant or an attenuated
CC Pasteurellaceae bacteria. The mutated genes have antibacterial activity
CC and can be used in vaccines. The gram-negative bacteria or the attenuated
CC Pasteurellaceae bacteria can be used as vaccines in the fields of human
CC medicine or veterinary medicine, and for identifying new antibacterial
CC agents that target the virulence genes and their products. ABQ83458 to
CC ABQ83578 and ABP54473 to ABP54551 represents sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 364 AA;

Query Match 36.8%; Score 671; DB 5; Length 364;
Best Local Similarity 42.4%; Pred. No. 2.3e-52;
Matches 153; Conservative 54; Mismatches 122; Indels 32; Gaps 10;

Qy 1 MKAIFVLNAAPKONTWYAGKLGWSQYHDTGFGYNGFQNNNGPTR----NDQLGAGAFGG 56
Db 131 VYGVKGIALVNNYKTFENAAQEKVKTRRFQS--SLILGAGVEYAILPELAARVEYQWLNN 188
```


Db 11 LSAAVAQAAPQONTFYAGAKAGWASPHDGIQLDSAKNTDRGTYKYGINRNSVTYGVFGG 70

Qy 57 YQV--NPYLGF--EMGYDMLGRM-----AYKGSVDNGAFK--AOGVOLTAKLGYPIITDLD 106

Db 71 YQILNQDKLGLAAELGYDFGRVGRSEKPNKADKTFRHAAGATIALKPSYEVLPDL 130

Qy 107 IYTRLG-GMVWRADSKGNVASTGVSRSHTDGVSPFAGGVAVTRDIATRLLEYQWNN 165

Db 131 VYGVKGIALVNNYTKTFNAAQEKVTRRFQS--SLILGAGVEYAILPELAARVEYQMLNN 188

Qy 166 IGDA-----GTGTRPDNGMLSLGVSRYFGQEDAAPVAPAPAPAPAVATKHFTLS 217

Db 189 AGKASYSTLNRMGATDYRSDISVSAGLSYRFQ--GAAPVAAPA-----VETKNFAFSS 241

Qy 218 DVLNFNKATLKPEGQQALDQYLTQLSNMDPKDSAVVLGYTDRIGSEAVNQQLSEKRAQ 277

Db 242 DVLFAFGKSLKPAATAALDAMQTEINNAGLSNAAIQVNGYTDRIKGEASNLKLSQRAE 301

Qy 278 SVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKE 337

Db 302 TVANYIVSKGAPAAVNTAVGGEANPVTGATCDKVKGRKALIACLAPDRRVEVQVQGTKE 361

Qy 338 V 338

Db 362 V 362

RESULT 43

AA97899

ID AA97899 standard; protein; 364 AA.

AC

AA97899;

DT 12-SEP-2003 (revised)

DT 11-SEP-2000 (first entry)

XX Actinobacillus pleuropneumoniae outer membrane protein, OmpA1.

XX OmpA1; outer membrane protein; APP; pneumonic pathogen; swine;

KW Sus scrofa; serotype; antigen; vaccine; cross-reactive immunity;

KW cross-protection; diagnosis.

XX Actinobacillus pleuropneumoniae; strain Pz419.

XX

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein /note= "Signal peptide"

FT 20..364

FT /note= "Mature OmpA1"

XX

XX EP1001025-A2.

XX

XX 17-MAY-2000.

XX

XX 20-OCT-1999; 99EP-00308262.

XX

XX 22-OCT-1998; 98US-0105285P.

XX

XX (PFIZ) PFIZER PROD INC.

XX

XX Ankenbauer RG, Baarsch MJ, Campos M, Keich RL, Rosey EL;

PI Warren-Stewart LM, Suiter BT;

XX

XX WPI; 2000-320438/28.

DR N-PSDB; AAA38557.

XX

XX Low molecular weight Actinobacillus pleuropneumoniae proteins and DNA

PT encoding them, for use as vaccines against the bacteria in swine.

XX

XX Claim 2; Fig 5; 81pp; English.

XX

XX This sequence represents a low molecular weight outer membrane protein,

CC OmpA1, from Actinobacillus pleuropneumoniae (APP) strain Pz419 (ATCC

CC 98929). The invention relates to the novel APP outer membrane proteins

CC Omp20, Omp27, OmpA1 and OmpA2 (AA97896-Y97900) and to nucleic

CC acids encoding them (AAA38554-A38558). APP is a Gram negative

CC coccobacillus which is one of the most important swine pneumonic

CC pathogens. 12 different serotypes of APP have been recognised which vary

CC in geographic distribution. Prior art attempts at vaccinating against APP

CC have produced mainly serotype-specific immune responses. In contrast,

CC natural immunity to any one serotype seems to confer significant

CC protection from disease caused by other serotypes, suggesting that

CC natural exposure induces cross-reactive immunity to shared antigens. The

CC novel outer membrane proteins of the invention are present in all 12

CC serotypes, and may provide a target for cross-protective immunisation.

CC The novel outer membrane proteins and nucleic acids encoding them can be

CC used as a vaccine against APP in swine. They can also be used as reagents

CC for the diagnosis of APP infections. (Updated on 12-SEP-2003 to

CC standardise OS field)

XX

SQ Sequence 364 AA;

Query Match 36.6%; Score 667; DB 3; Length 364;

Best Local Similarity 42.1%; Pred. No. 5.3e-52;

Matches 152; Conservative 54; Mismatches 123; Indels 32; Gaps 10;

Qy 1 MKAIFVLNAPKONTWTYAGKLGWSQVHDTGTFYNGFQNNNGPTR----NDQLGAGAFGG 56

Db 11 LSAAVAQAAPQONTFYAGAKAGWASPHDGIQLDSAKNTDRGTYKYGINRNSVTYGVFGG 70

Qy 57 YQV--NPYLGF--EMGYDMLGRM-----AYKGSVDNGAFK--AOGVOLTAKLGYPIITDLD 106

Db 71 YQILNQDKLGLAAELGYDFGRVGRSEKPNKADKTFRHAAGATIALKPSYEVLPDL 130

Qy 107 IYTRLG-GMVWRADSKGNVASTGVSRSHTDGVSPFAGGVAVTRDIATRLLEYQWNN 165

Db 131 VYGVKGIALVNNYTKTFNAAQEKVTRRFQS--SLILGAGVEYAILPELAARVEYQMLNN 188

Qy 166 IGDA-----GTGTRPDNGMLSLGVSRYFGQEDAAPVAPAPAPAVATKHFTLS 217

Db 189 AGKASYSTLNRMGATDYRSDISVSAGLSYRFQ--GAAPVAAPA-----VETKNFAFSS 241

Qy 218 DVLNFNKATLKPEGQQALDQYLTQLSNMDPKDSAVVLGYTDRIGSEAVNQQLSEKRAQ 277

Db 242 DVLFAFGKSLKPAATAALDAMQTEINNAGLSNAAIQVNGYTDRIKGEASNLKLSQRAE 301

Qy 278 SVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKE 337

Db 302 TVANYIVSKGAPAAVNTAVGGEANPVTGATCDKVKGRKALIACLAPDRRVEVQVQGTKE 361

Qy 338 V 338

Db 362 V 362

RESULT 44

AA96097

ID AA96097 standard; protein; 364 AA.

XX

XX AA96097;

XX

XX 19-DEC-2000 (first entry)

XX

XX Actinobacillus pleuropneumoniae OmpA1.

DE

XX Outer membrane protein; OmpA1; vaccine; pig; immunogen;

KW dual immune response; immunogen; pleuropneumonia.

KW

XX Actinobacillus pleuropneumoniae.

OS

XX EP1035133-A2.

PN

XX 13-SEP-2000.

PD

XX 14-FEB-2000; 2000EP-00301103.

CC

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PR 17-FEB-1999; 99US-012045AP.
XX (PFIZ ) PFIZER PROD INC.
XX Campos M, Martinod SR, Durtschi BA, Yule TD;
XX WPI; 2000-566924/53.
XX
XX Novel fusion protein for producing a dual immune response comprises a
XX peptide analogous to an endogenous peptide which is to be inhibited,
XX connected to a peptide analogous to an immunogen from a pathogen which
XX infects a vertebrate.
XX
XX Disclosure; Page 57-58; 93pp; English.
XX
XX The present sequence is that of outer membrane protein OmpA1 of
XX Actinobacillus pleuropneumoniae. OmpA1 can be utilised in fusion proteins
XX of the invention that are used as vaccines eliciting a dual immune
XX response. Such fusion proteins comprise: a first protein that is
XX endogenous to a vertebrate, the activity of which is to be inhibited
XX within the vertebrate, and which is incapable by itself of eliciting an
XX effective immunoinhibitory response in the vertebrate; and a second
XX protein, which is an immunogen from a pathogen capable of infecting the
XX vertebrate, and which causes the vertebrate's immune system to recognise
XX the first protein, producing a response that inhibits the activity of the
XX first protein, and also protecting the vertebrate from infection by the
XX pathogen when the vertebrate is vaccinated with the fusion protein. In
XX the present case, a fusion protein of cholecystokinin and OmpA1 is useful
XX for encouraging appetite in swine while simultaneously providing a
XX protective immune response against porcine pleuropneumonia
XX
XX Sequence 364 AA;
XX
XX Query Match 36.6%; Score 667; DB 3; Length 364;
XX Best Local Similarity 42.1%; Pred. No. 5.3e-52;
XX Matches 152; Conservative 54; Mismatches 123; Indels 32; Gaps 10;
XX
XX 1 MKAFVLNNAAPKDNNTWYAGGKLGWSQYHDTGFGNGFONNNGPTR----NDQLGAGAFGG 56
XX 11 LSAAVAQAAPQONTFYAGAKAGWASFHDGIEQLDSAKNTDRGTRYGINNSVTYGVFGG 70
XX
XX 57 YQV--NPYLGF--ENGVDWLGFM-----AYKGSVDNGAFK--AQGVQLTAKLGYPTDLDL 106
XX 71 YQILNQDLGLAAELGYDYFGRVRSKXPGKADKTRHAAHGATIALKPSYEVLPDL 130
XX
XX 107 IYTRLG-GMNVRAADSKGNVASTGVSRSSEHDTGVSFVAGGVEMAVTRDIATRLLEYQWNN 165
XX 131 VYGVKGVIALVNNYKTFNAAQEKVTRRFQS--SLILGAGVEYAILPELAARVEYQMLNN 188
XX
XX 166 IGDA-----GTGTRPDNGMLSLGVSRYRFGQEDAAPVVAAPAPAPAPEVATKHTLKS 217
XX 189 AKGASYSTLNRMGATDYKRSDDISSVAGUSYRFGQ-GAVPVAAPA-----VETKNFAPSS 241
XX
XX 218 DVLNFKATLKPEGQQALDOLYTOLSNMDPKDGSVAVLGYTDRIGSEAYNQOLSEKRAQ 277
XX 242 DVLFAFGSNLKPAAATLADAMQTEINNAGLSNRAIQVNGYTDRLGKEASNLKSORRAE 301
XX
XX 278 SVVDYLVAKGIPAGKISARGMESNPVTGNTCDNVKARAALIDCLAPRRVEIEVKGYKE 337
XX 302 TVANYIVSKGAPAAANVTAVGGEANPVTGATCDYKVKRKALIACLAPRRVEVQVQGTKE 361
XX
XX 338 V 338
XX 362 V 362
XX
XX RESULT 45
XX AAR66294
XX ID AAR66294 standard; protein; 359 AA.
XX
XX AAR66294;
XX
XX 27-AUG-2003 (revised)

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DT 25-MAR-2003 (revised)
DT 09-AUG-1995 (first entry)
XX
XX Non-typable Haemophilus influenza (NTHi) fimbrin protein.
XX Fimbrin protein; vaccine; otitis media.
XX
XX Haemophilus influenzae.
XX
XX Key Location/Qualifiers
XX FH 22..33
XX Region /label= amino terminus
XX FT Peptide 234..249
XX /label= internal CNBr fragment
XX
XX W09426304-A1.
XX
XX 24-NOV-1994.
XX
XX 12-MAY-1994; 94WO-US005477.
XX
XX 18-MAY-1993; 93US-00065442.
XX
XX (OHIS ) UNIV OHIO STATE RES FOUND.
XX
XX Kolattukudy PE, Bakaletz LO, Sirakova T;
XX WPI; 1995-006359/01.
XX N-PSDB; AAO78916.
XX
XX Vaccine comprising non-typable Haemophilus influenza fimbrin protein -
XX useful in studying, preventing or reducing the severity of otitis media,
XX also fimbrin protein and DNA.
XX
XX Disclosure; Fig 5; 45pp; English.
XX
XX The fimbrin proteins from 15 randomly selected type b and non- typable
XX clinical isolates of Haemophilus influenzae share common epitopes. Thus
XX fimbrin isolated from non-typable Haemophilus influenzae 1128 strain is
XX particularly suitable immunogen to protect against the different non-
XX typable H3. influenzae that cause otitis media. Fimbrin protein is
XX produced by culturing a transformed microbial host , pref. E.coli,
XX Sporodoptera frugiperda or a mucosal pathogen. Fimbrin protein (Fp)
XX produced by this process is claimed. The Fp protein migrates in
XX polyacrylamide gels to a posn. equiv. to a mol. wt. of 25.5 kD or 37.5
XX kD. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003
XX to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 359 AA;
XX
XX Query Match 36.0%; Score 655.5; DB 2; Length 359;
XX Best Local Similarity 43.0%; Pred. No. 5.9e-51;
XX Matches 154; Conservative 49; Mismatches 122; Indels 33; Gaps 9;
XX
XX 1 MKAFVLNNAAPKDNNTWYAGGKLGWSQYHDTGFGNGFONNNGPTRNDQLGAGAFGG 56
XX 13 LAAASVAQAAPQONTFYAGKAGGSGFHDGINNGAIAKGLSSSNVGYRRTFTYGVFGG 72
XX
XX 57 YQV-----NPYLGFEMGYDWLGRMAYKGSVDNGAFKAQ-----GVQLTAKLGYPTDLDLIY 108
XX 73 YQILNQDNFGLAAELGYHDFGRAKLR---EAGKPKAKHTNHGAYLSLKGSYEVLDGLDVY 129
XX
XX 109 TRLGGMVWRADSKGNVASTGV---SRSEHDTGVSFVAGGVEMAVTRDIATRLLEYQWNN 165
XX 130 GKAGVALVRSYDKFYEDANGTRDHKGRHTARASGLFAVGAAYVLPVLAARVYQMLTR 189
XX
XX 166 IG-----DAGTVGTRPDNGMLSLGVSRYRFGQDAAAPVVAAPAPAPAPEVATKHTLKS 218
XX 190 VGKYPQDKPNTAINYNPWGICINAGISYRFGQE-APVVA-----APWYSKTFSLNSD 243
XX
XX 219 VLFNFKATLKPEGQQALDOLYTOLSNMDPKDGSVAVLGYTDRIGSEAYNQOLSEKRAQ 278
XX 244 VTFAGKANLKPAQAATLDSVYGEISQV--KSRKVAVAGYTNRIGSDFAFNVKLSQERADS 301

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Db 13 LAAASVAQAAPQENTFYAGVKAGQASFDH-GLRALAREKNVGYHRN-SFTYGVFGGYQIL 70

PS Disclosure: Fig 1: 29pp: English.


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XX PF 17-JAN-2002; 2002WO-US001971.
XX PR 15-MAR-2001; 2001US-00809665.
XX PA (PHAA ) PHARMACIA & UPJOHN CO.
XX PI Lowery DE, Fuller TE, Kennedy MJ;
XX DR WPI; 2002-740868/80.
XX DR N-PSDB; ABQ83541.
XX PT New mutant gram-negative bacteria, useful as vaccines and for identifying
XX PT new anti-bacterial agents that target virulence genes and their products.
XX PS Claim 36; Page 314-315; 350pp; English.
XX CC The present invention describes a gram-negative bacteria comprising a
XX CC mutation in a gene, where the mutation results in decreased activity of a
XX CC gene product encoded by the mutated gene. Also described is a method for
XX CC producing a gram-negative bacteria mutant or an attenuated
XX CC Pasteurellaceae bacteria. The mutated genes have antibacterial activity
XX CC and can be used in vaccines. The gram-negative bacteria or the attenuated
XX CC Pasteurellaceae bacteria can be used as vaccines in the fields of human
XX CC medicine or veterinary medicine, and for identifying new antibacterial
XX CC agents that target the virulence genes and their products. ABQ83458 to
XX CC ABQ83578 and ABP54473 to ABP54551 represents sequences used in the
XX CC exemplification of the present invention
XX SQ Sequence 369 AA;

Query Match 35.5%; Score 646.5; DB 5; Length 369;
Best Local Similarity 41.1%; Pred. No. 4e-50;
Matches 153; Conservative 60; Mismatches 110; Indels 49; Gaps 12;

Qy 1 MKAIFVLNAAAPKDNWTYAGKLGWSQYHDTGFGY-NGFQNNNGPTRNDQ-----L 49
Db 11 LSAAVAQAAPQONTFYAGAKVGQSSPH----HGVNQLKSGHDDRYNDKTRKYGINRNSV 66
Qy 50 GAGAFGGYQV----NPYLGFEMGVDWLCRMAYKGSVDNGAFK-----AOGVOLTAKLGYP 100
Db 67 TYGVFGGYQIILNQNNFGLAELGYDYGRV--RGNVDE--FRTVKHSHAGLNALKFSYE 122
Qy 101 ITDDLDIYTRLGGVMWRADSKGNVASTGVSRSE---HDTGVSPVPFAGVVEAVTRDIATR 157
Db 123 VLPDLGVYKGVIAVRNDYK-KYGAENTNESTTKFKHLKASTILGAGVEVAILPELAAR 181
Qy 158 LEYQWVNNIGDAGTV----GTR-----PDNGMLSLGVSYRFGQEDAAPVVAAPAPAP 206
Db 182 VEYQYLNKAGNLKALVRSQTDVDFQYAPDIHSVTAGLSYRFGQGAAPVW-----EP 235
Qy 207 EVATKFTLKSDDLFLNFENKATLKPEGQALDQLYTOLSNMDDPKDGSVVILGYTDRIGSEA 266
Db 236 EVVTKNFAFSSDVLDFDKSKSLKPAATALDAANTETANUGLATPALTQVNGYTDRIKREA 295
Qy 267 YNOQLSEKRAQSVVDLYLVAKIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDR 326
Db 296 SNLKSQRRAETVANYLVSKQNPANVTAVGYGEANPVTGATCDVAKGRKALIACLAPDR 355
Qy 327 RVEIEVKGKGV 338
Db 356 RVEVQVQAGKNV 367

RESULT 50
AA97900
ID AA97900 standard; protein; 369 AA.
XX
XX AA97900;
AC
XX
AC
XX
DT 12-SEP-2003 (revised)
DT 11-SEP-2000 (first entry)
XX

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```

DE Actinobacillus pleuropneumoniae outer membrane protein, OmpA2.
XX
KW OmpA2; outer membrane protein; APP; pneumonic pathogen; swine;
KW Sus scrofa; serotype; antigen; vaccine; cross-reactive immunity;
KW cross-protection; diagnosis.
XX
OS Actinobacillus pleuropneumoniae; strain Pz420.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "Signal peptide"
FT Protein 20..369
FT /note= "Mature OmpA2"
XX
PN EP1001025-A2.
XX
XX 17-MAY-2000.
XX
XX 20-OCT-1999; 99EP-00308262.
XX
XX 22-OCT-1998; 98US-0105285P.
XX
XX (PFIZ ) PFIZER PROD INC.
XX
XX Ankenbauer RG, Baarsch MJ, Campos M, Keich RL, Rosey EL;
XX Warren-Stewart LM, Suiter BT;
XX WPI; 2000-320438/28.
XX N-PSDB; AAA38558.
XX
XX Low molecular weight Actinobacillus pleuropneumoniae proteins and DNA
XX encoding them, for use as vaccines against the bacteria in swine.
XX
XX Claim 2; Fig 5; 81pp; English.
XX
XX This sequence represents a low molecular weight outer membrane protein,
XX OmpA2, from Actinobacillus pleuropneumoniae (APP) strain Pz420 (ATCC
XX 9830). The invention relates to the novel APP outer membrane proteins
XX Omp20, OmpW, Omp27, OmpA1 and OmpA2 (AA97986-97990) and to nucleic
XX acids encoding them (AAA38554-A38558). APP is a Gram negative
XX coccobacillus which is one of the most important swine pneumonic
XX pathogens. 12 different serotypes of APP have been recognised which vary
XX in geographic distribution. Prior art attempts at vaccinating against APP
XX have produced mainly serotype-specific immune responses. In contrast,
XX natural immunity to any one serotype seems to confer significant
XX protection from disease caused by other serotypes, suggesting that
XX natural exposure induces cross-reactive immunity to shared antigens. The
XX novel outer membrane proteins of the invention are present in all 12
XX serotypes, and may provide a target for cross-protective immunisation.
XX The novel outer membrane proteins and nucleic acids encoding them can be
XX used as a vaccine against APP in swine. They can also be used as reagents
XX for the diagnosis of APP infections. (Updated on 12-SEP-2003 to
XX standardise OS field)
XX
XX Sequence 369 AA;

Query Match 35.1%; Score 639.5; DB 3; Length 369;
Best Local Similarity 40.7%; Pred. No. 1.8e-49;
Matches 151; Conservative 60; Mismatches 113; Indels 47; Gaps 11;

Qy 1 MKAIFVLNAAAPKDNWTYAGKLGWSQYHDTGFGY-NGFQNNNGPTRNDQ-----L 49
Db 11 LSAAVAQAAPQONTFYAGAKVGQSSPH----HGVNQLKSGHDDRYNDKTRKYGINRNSV 66
Qy 50 GAGAFGGYQV----NPYLGFEMGVDWLCRMAYKGSVDNGAFK-----AOGVOLTAKLGYP 100
Db 67 TYGVFGGYQIILNQNNFGLAELGYDYGRV--RGNVDE--FRTVKHSHAGLNALKFSYE 122
Qy 101 ITDDLDIYTRLGGVMWRADSKGNVASTGVSRSE---HDTGVSPVPFAGVVEAVTRDIATR 158
Db 123 VLPDLGVYKGVIAVRNDYK-KYGAENTNESTTKFKHLKASTILGAGVEVAILPELAAR 182
Qy 159 EYQWVNNIGDAGTV----GTR-----PDNGMLSLGVSYRFGQEDAAPVVAAPAPAPE 207

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Db 183 EYQVNLKAGNLKALVRSQTQDVFQYAPDIHSVTAGLSYRFGGAVPVV-----EPE 236
Qy 208 VATKHTLKSVDLNFENKATLKPEGOALDQLYTQLSNMOPKGSVAVLGYTDRIQSEAY 267
Db 237 VVTKNFAFSSDVLDFGKSSLKPAATAALDAANTEIANGLATPAIQVNGYTDRIQSEAS 296
Qy 268 NQOLSEKRAQSVVDYLVAKGTPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRR 327
Db 297 NLKLSQRRRAETVANYLVSKGQNPANVTAVGYGEANPVTGATCDKVKGRKALIACLAPDRR 356
Qy 328 VEIEVKGYKEV 338
Db 357 VEVOVQGAQNV 367

RESULT 51
AA96098
ID AAY96098 standard; protein; 369 AA.

XX AC AAY96098;

XX DT 19-DEC-2000 (first entry)

XX DE Actinobacillus pleuropneumoniae OmpA2.

XX KW Outer membrane protein; OmpA1; vaccine; pig; immunogen;
XX dual immune response; immunogen; pleuropneumonia.

XX OS Actinobacillus pleuropneumoniae.

XX PN EP1035133-A2.

XX PD 13-SEP-2000.

XX PF 14-FEB-2000; 2000EP-00301103.

XX PR 17-FEB-1999; 99US-0120454P.

XX PA (PFIZ) PFIZER PROD INC.

XX PI Campos M, Martinod SR, Durtschi BA, Yule TD;

XX DR WPI; 2000-566924/53.

XX PT Novel fusion protein for producing a dual immune response comprises a
PT peptide analogous to an endogenous peptide which is to be inhibited,
PT connected to a peptide analogous to an immunogen from a pathogen which
PT infects a vertebrate.

XX PS Disclosure; Page 58-60; 93pp; English.

XX CC The present sequence is that of outer membrane protein OmpA2 of
CC Actinobacillus pleuropneumoniae. OmpA2 can be utilised in fusion proteins
CC of the invention that are used as vaccines eliciting a dual immune
CC response. Such fusion proteins comprise: a first protein that is
CC endogenous to a vertebrate, the activity of which is to be inhibited
CC within the vertebrate, and which is incapable by itself of eliciting an
CC effective immunoinhibitory response in the vertebrate; and a second
CC protein, which is an immunogen from a pathogen capable of infecting the
CC vertebrate, and which causes the vertebrate's immune system to recognise
CC the first protein, producing a response that inhibits the activity of the
CC first protein, and also protecting the vertebrate from infection by the
CC pathogen when the vertebrate is vaccinated with the fusion protein. In
CC the present case, a fusion protein of cholecystokinin and OmpA2 is useful
CC for encouraging appetite in swine while simultaneously providing a
CC protective immune response against porcine pleuropneumonia

XX CC Sequence 369 AA;

Query Match 35.1%; Score 639.5; DB 3; Length 369;
Best Local Similarity 40.7%; Pred. No. 1.8e-49;
Matches 151; Conservative 60; Mismatches 113; Indels 47; Gaps 11;

Qy 1 MKAIFVLNRAAPKONTWAGCKLQWSQYHDTGTFYG-NGFQNNNGPTRNDQ-----L 49
Db 11 LSAAVAQAAPQONTFYAGAKVGQSSFH---HGVNOLKSGHDDRYNDKTRKYGINRNSV 66
Qy 50 GAGAGGYQV---NPYLGFEMGYDMLGRMAYKGSVDNGAFK-----AQGVQLTAKLGYP 100
Db 67 TYGVFGYQILNQNNFGLATLGYDYGRV--RG--NDGEFRAMKHSAGHNFALKPSYE 122
Qy 101 ITDDLITYTLGGMWRADSKGNVASTGVSRSB--HDTGVSVPVAGGVWAVTRDIATRL 158
Db 123 VLPDLVYGVGVAVVRNDYKSYCAENTNEPTKEFKHLKASTILGAGVEYAILPELAARV 182
Qy 159 EYQWVNNIGDAGTV---GTR-----PDNGMLSLGVSYRFGQEDAAPVVPAPAPAPE 207
Db 183 EYQVNLKAGNLKALVRSQTQDVFQYAPDIHSVTAGLSYRFGGAVPVV-----EPE 236
Qy 208 VATKHTLKSVDLNFENKATLKPEGOALDQLYTQLSNMOPKGSVAVLGYTDRIQSEAY 267
Db 237 VVTKNFAFSSDVLDFGKSSLKPAATAALDAANTEIANGLATPAIQVNGYTDRIQSEAS 296
Qy 268 NQOLSEKRAQSVVDYLVAKGTPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRR 327
Db 297 NLKLSQRRRAETVANYLVSKGQNPANVTAVGYGEANPVTGATCDKVKGRKALIACLAPDRR 356
Qy 328 VEIEVKGYKEV 338
Db 357 VEVOVQGAQNV 367

RESULT 51
ADM20161
ID ADM20161 standard; protein; 157 AA.

XX AC ADM20161;

XX DT 20-MAY-2004 (first entry)

XX DE Protein encoded by novel human channel/transporter gene #281 clone 2.

XX KW immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
KW gene therapy; channel/transporter protein; rheumatoid arthritis;
KW neoplasm; cardiac arrest; cerebrovascular disorder; cerebral ischemia;
KW angiogenesis; nervous system disorder; Alzheimer's disease;
KW ocular disorder; corneal infection; wound healing;
KW epithelial cell proliferation; skin aging; sunburn; transplantation;
KW chemotaxis; food additive.

XX OS Homo sapiens.

XX PN WO200154472-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001307.

XX PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.

Db 1 TGVSPVFAGGVEWAVTRDIATRLRYQWVNIGDAGTGTCTRPDNGMLSLGVSyr 53

RESULT 57
ABG91067
ID ABG91067 standard; protein; 236 AA.
AC ABG91067;
XX
XX 29-NOV-2002 (first entry)
XX
XX Neisseria gonorrhoeae gonococcal protein III protein.
XX
XX Gram-negative bacterial bleb; PorB; outer membrane protein;
KW Chlamydia trachomatis infection; Chlamydia pneumoniae infection;
KW protective antigen; antibacterial; vaccine.
XX
XX Neisseria gonorrhoeae.
XX
XX WO200262380-A2.
XX
XX 15-AUG-2002.
XX
XX 08-FEB-2002; 2002WO-EP001356.
XX
XX 08-FEB-2001; 2001GB-00003169.
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Berthet FU, Lobet Y, Poolman J, Verlant VGCL;
XX
XX WPI; 2002-657510/70.
XX N-PSDB; ABS67386.
XX
XX Novel gram-negative bacterial bleb presenting on its surface PorB outer
PT membrane protein from Chlamydia trachomatis or protective antigen from
PT Chlamydia pneumoniae, useful for preventing Chlamydia infection.
XX
XX Disclosure; Page 58; 75pp; English.
XX
XX The present invention relates to a new gram-negative bacterial bleb
CC presenting on its surface the PorB outer membrane protein from Chlamydia
CC trachomatis, or a protective antigen from C. pneumoniae. The invention is
CC useful for preventing C. trachomatis or C. pneumoniae infection in a
CC host. The present amino acid sequence represents a Neisseria gonorrhoeae
CC protein as described in the invention
XX
XX Sequence 236 AA;
Query Match 14.4%; Score 262; DB 5; Length 236;
Best Local Similarity 35.0%; Pred. No. 2.8e-15;
Matches 69; Conservative 29; Mismatches 67; Indels 32; Gaps 6;
Qy 164 NNIGDA--GTVGTRPDNGMLSLGVSyrFGQSDAAPVVPAPAP-----APEVATKHFTL 215
Db 42 NNYGECWKNAYFDKASQGRVECG-----DAVAVPEPEPAPVAVVEQAPQYVDETISL 93
Qy 216 KSDVLFNFKATLKPEGQQAALDQLYTQLSNMDPKDGSAVLGYTDRIGSEAYNQOLSEKR 275
Db 94 SAKTLFGFDKDSLRAEAQDNLKVLQAQLSRNTVQ--SVRVEGHTDFMGSEKYNQALSERR 151
Qy 276 AQSVDVYLVAKGIPAGKISARGMGESNPVTGNTC-----DNNKAAALIDCLAP 324
Db 152 AYVANNLVNGVPASRISAVGLGESQAQMTQVCOAEVAKLGAKAKKKEALIACTIEP 211
Qy 325 DRRVEIEVKGYKEVVTQ 341
Db 212 DRRVDVKI---RSIVTR 225
RESULT 58
ABP80776
ID ABP80776 standard; protein; 236 AA.

XX ABP80776;
XX
XX 07-MAR-2003 (first entry)
XX
XX N. gonorrhoeae amino acid sequence SEQ ID 8082.
XX
XX Antibacterial; infection; vaccine; gene therapy.
XX
XX Neisseria gonorrhoeae.
XX
XX WO200279243-A2.
XX
XX 10-OCT-2002.
XX
XX 12-FEB-2002; 2002WO-IB002069.
XX
XX 12-FEB-2001; 2001GB-00003424.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Fontana MR, Pizza M, Masignani V, Monaci E;
XX
XX WPI; 2003-058415/05.
XX N-PSDB; ABZ41746.
XX
XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a
PT medicament for treating or preventing N. gonorrhoeae infection.
XX
XX Disclosure; Page 778; 815pp; English.
XX
XX The present invention relates to proteins from Neisseria gonorrhoeae.
CC Also disclosed are the nucleic acid molecules encoding the proteins and
CC antibodies that specifically bind to the proteins. The composition
CC comprising the protein, nucleic acid or antibody is useful for the
CC manufacture of a medicament for treating or preventing N. gonorrhoeae
CC infection, this may be in the form of a vaccine or gene therapy.
CC
CC Sequences given in records ABP76736-ABP81046 represent nucleic acid
CC molecules of the invention
XX
XX Sequence 236 AA;
Query Match 14.4%; Score 262; DB 6; Length 236;
Best Local Similarity 35.0%; Pred. No. 2.8e-15;
Matches 69; Conservative 29; Mismatches 67; Indels 32; Gaps 6;
Qy 164 NNIGDA--GTVGTRPDNGMLSLGVSyrFGQSDAAPVVPAPAP-----APEVATKHFTL 215
Db 42 NNYGECWKNAYFDKASQGRVECG-----DAVAVPEPEPAPVAVVEQAPQYVDETISL 93
Qy 216 KSDVLFNFKATLKPEGQQAALDQLYTQLSNMDPKDGSAVLGYTDRIGSEAYNQOLSEKR 275
Db 94 SAKTLFGFDKDSLRAEAQDNLKVLQAQLSRNTVQ--SVRVEGHTDFMGSEKYNQALSERR 151
Qy 276 AQSVDVYLVAKGIPAGKISARGMGESNPVTGNTC-----DNNKAAALIDCLAP 324
Db 152 AYVANNLVNGVPASRISAVGLGESQAQMTQVCOAEVAKLGAKAKKKEALIACTIEP 211
Qy 325 DRRVEIEVKGYKEVVTQ 341
Db 212 DRRVDVKI---RSIVTR 225
RESULT 59
ABG80415
ID ABG80415 standard; protein; 242 AA.
AC ABG80415;
XX
XX 29-NOV-2002 (first entry)
XX
XX Neisseria meningitidis strain MC58 rmpM protein.
XX

KW Hyperblebbing; Gram-negative bacterium; genetically modified; Tol gene;
 KW peptidoglycan-binding; peptidoglycan-associated site; outer-membrane;
 KW bacterial infection; vesicle-shedding; bleb; filter sterilised;
 KW detergent; deoxycholate; homogeneity; antibacterial; vaccine; exbB; exbD;
 KW rmpM.

XX *Neisseria meningitidis*.

XX WO200262378-A2.

XX 15-AUG-2002.

XX 08-FEB-2002; 2002WO-EP001361.

XX 08-FEB-2001; 2001GB-00003171.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Berthet FJ, Denoel P, Neyt CA, Poolman J, Thonnard J;

XX WPI; 2002-657509/70.

XX N-PSDB; ABS66188.

XX Novel hyperblebbing Gram-negative bacterium that has been genetically
 PT modified by down-regulating expression of Tol genes, and/or attenuating
 PT peptidoglycan-binding activity useful for treating bacterial infection.

XX Disclosure; Page 54; 71pp; English.

XX The present invention relates to a new hyperblebbing Gram-negative
 CC bacterium genetically modified by one or more Tol processes selected from
 CC down-regulating expression of one or more Tol genes and attenuating the
 CC peptidoglycan-binding activity by mutation of one or more gene(s)
 CC encoding a protein comprising a peptidoglycan-associated site. The
 CC invention is useful in a method of treatment of the human or animal body.
 CC The invention is also useful for protecting an individual against a
 CC bacterial infection. The invention has improved outer-membrane vesicle-
 CC shedding properties. Blebs are more easily made in higher yield from the
 CC invention, and are more homogeneous in nature and can be more readily
 CC filter sterilised. The blebs can be made and harvested without the use of
 CC detergents such as deoxycholate, thus obviating chromatography
 CC purification and ultra centrifugation steps. Vesicles prepared from the
 CC invention have reduced particle size (allowing sterile filtration through
 CC 0.22 µm pores), increased batch homogeneity, and a superior yield. The
 CC present amino acid sequence represents a *Neisseria meningitidis*
 CC protein, as described in the invention

XX Sequence 242 AA;

Query Match 14.0%; Score 255; DB 5; Length 242;
 Best Local Similarity 33.3%; Pred. No. 1.3e-14;
 Matches 65; Conservative 34; Mismatches 74; Indels 22; Gaps 5;
 QY 164 NNIGDA--GTVGTRPDNGMLSLGVSYRFGQEDAAPVAPAPA----PAPEVATKHFTLKS 217
 DB 42 NNYGECWKNAYFDKASQGRVECGDAVAAPPEPEPEPAPVWVVEQAPQVDETISLSA 101
 QY 218 DVLFNFNKATLKPEGQQAALDQLYTOLSNMDDPKGSAAVVLGYTDRIGSEAYNQQLSEKRAQ 277
 DB 102 KTLFGFDKDSLRAEADQNLKVLQRLSRNTVQ--SVRVEGHTDFMGSDKYNQALSERRAY 159
 QY 278 SVVDYLVAKGIPAGKISARGMGESNPVTGNTCD-----NVKAAALIDCLAPDR 326
 DB 160 VVANNLVSGVPVSRISAVLGESQAQMTQVCEAEVAKLGAKVSKAKKREALIACIEPDR 219
 QY 327 RVEIEVKGYKEVVTQ 341
 DB 220 RVDVKI---RSIVTR 231

RESULT 60

ID ADP08212

ID ADP08212 standard; protein; 242 AA.

XX

ADP08212;

XX 26-AUG-2004 (first entry)

XX *Neisseria meningitidis* MC58 OMV-related membrane protein - SEQ ID 45.

XX outer-membrane vesicle; antibacterial; antiinflammatory;

XX meningococcal protein trafficking; localisation; infection; vaccine;
 KW gene therapy.

XX *Neisseria meningitidis* MC58.

XX WO2004046177-A2.

XX 03-JUN-2004.

XX 17-NOV-2003; 2003WO-IB006281.

XX 15-NOV-2002; 2002GB-00026734.

XX 27-MAR-2003; 2003GB-00007131.

XX (CHIR) CHIRON SRL.

XX Norais N, Grandi G;

XX WPI; 2004-420615/39.

XX New compositions having outer-membrane vesicles and proteins from

XX *Neisseria meningitidis*, useful in the field of meningococcal
 PT biochemistry, in particular for preventing and/or treating meningococcal
 PT infections.

XX Claim 9; SEQ ID NO 45; 79pp; English.

XX The invention relates to a novel composition comprising outer-membrane
 CC vesicles (OMV) prepared from a first strain of *Neisseria meningitidis* and
 CC 1 or more proteins which are present in OMVs prepared from a second
 CC strain of *N. meningitidis*, but which are not present in OMVs prepared
 CC from the first strain. The composition of the invention demonstrates
 CC antibacterial and antiinflammatory activities and may be useful in the
 CC field of meningococcal biochemistry, in particular the trafficking and
 CC localisation of meningococcal proteins, as well as in the prevention of a
 CC treatment of meningococcal infections, possibly via the production of a
 CC vaccine or gene therapy. The current sequence is that of a *Neisseria*
 CC meningitidis MC58 outer-membrane vesicle (OMV)-related membrane protein
 CC of the invention.

XX Sequence 242 AA;

Query Match 14.0%; Score 255; DB 8; Length 242;
 Best Local Similarity 33.3%; Pred. No. 1.3e-14;
 Matches 65; Conservative 34; Mismatches 74; Indels 22; Gaps 5;
 QY 164 NNIGDA--GTVGTRPDNGMLSLGVSYRFGQEDAAPVAPAPA----PAPEVATKHFTLKS 217
 DB 42 NNYGECWKNAYFDKASQGRVECGDAVAAPPEPEPEPAPVWVVEQAPQVDETISLSA 101
 QY 218 DVLFNFNKATLKPEGQQAALDQLYTOLSNMDDPKGSAAVVLGYTDRIGSEAYNQQLSEKRAQ 277
 DB 102 KTLFGFDKDSLRAEADQNLKVLQRLSRNTVQ--SVRVEGHTDFMGSDKYNQALSERRAY 159
 QY 278 SVVDYLVAKGIPAGKISARGMGESNPVTGNTCD-----NVKAAALIDCLAPDR 326
 DB 160 VVANNLVSGVPVSRISAVLGESQAQMTQVCEAEVAKLGAKVSKAKKREALIACIEPDR 219
 QY 327 RVEIEVKGYKEVVTQ 341
 DB 220 RVDVKI---RSIVTR 231

RESULT 61

ADM94937


```
Db      297 GESRPVADNATEAGR-----AVNRRVEASVE 322
RESULT 63
ADA33932
ID      ADA33932 standard; protein; 379 AA.
XX
AC      ADA33932;
XX
DT      20-NOV-2003 (first entry)
XX
DE      Acinetobacter baumannii protein #1093.
XX
KW      Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
KW      plant biocontrol agent.
XX
OS      Acinetobacter baumannii.
XX
FN      US6562958-B1.
XX
PD      13-MAY-2003.
XX
PF      04-JUN-1999; 99US-00328352.
XX
PR      09-JUN-1998; 99US-0088701P.
XX
PA      (GENO-) GENOME THERAPEUTICS CORP.
XX
PI      Breton G, Bush D;
XX
WPI; 2003-576092/54.
DR      N-PSDB; ADA29806.
XX
XX      New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
PT      for diagnosing a bacterial disease, as components of antibacterial
PT      vaccines, as targets for antibacterial drugs, or as biocontrol agents for
PT      plants.
XX
PS      Example; SEQ ID NO 5219; 328pp; English.
XX
XX      The invention relates to isolated Acinetobacter baumannii nucleic acids.
CC      The A. baumannii nucleic acids and polypeptides are useful as reagents
CC      for diagnosing a bacterial disease, as components of antibacterial
CC      vaccines, as targets for antibacterial drugs, to detect the presence of
CC      A. baumannii and other Acinetobacter species in a sample, in screening
CC      compounds for the ability to interfere with the A. baumannii life cycle
CC      or to inhibit A. baumannii infection, and as biocontrol agents for
CC      plants. The present sequence represents the amino acid sequence of an A.
CC      baumannii protein.
XX
SQ      Sequence 379 AA;
Query Match      13.3%; Score 242.5; DB 6; Length 379;
Best Local Similarity 26.1%; Pred. No. 3.3e-13;
Matches 91; Conservative 55; Mismatches 138; Indels 65; Gaps 12;
Qy      22 LGWSQYHDTFGYNGFQFQ---NNGPTRNDQLGAGAFGGYQVNPVLGFMGYDMLGRMAYK 78
Db      57 LGYT-FQDTQ-HNNGGKDGELTNGPELQDDLFGAALGIELTPWLGFPEAYNQV-----K 109
Qy      79 GSDVNGAFKAGGVQLTAKLGYPIITDDL-----DIYTRLGG-----MVWRADS 120
Db      110 GDVDGLAAGAEYKQKQINGNFVYTSDLITKNYDSKIRPYVLGAGHYKYEIPDLSYHNDE 169
Qy      121 KGNVASTGVSRSEHDTGVSVPFAGVVEWATRDIAIRLEYQWVNNIGDAGTVGTRPDNGM 180
Db      170 EGTGLNAGV-----GAFWRLNDALSRLTEARGTYNFDKFNMTY-----AL 210
Qy      181 LSLGVSYRFGQEDAAPVVAAP-----APAEVATKHFTLKSVDLNFENKATLKPEGOQ 234
Db      211 AGLNVILGGHUKPAPVVEVAPVEPTVPAPQFQBELDLNMLVFFDTNKSNIKQDKP 270
Qy      235 ALDQLYTQLSNMDPKDGSVAVVLGYTDRIGSEAYNQQLSEKRAQSQSVVDYLVAK-GIPAGKI 293

Db      271 EIAKVAEKLS--EYPNATARIEGHTDNTGPKLNERLSLARANSVKGALVNEYNVDASRL 328
Qy      294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRVEIEVKGYKEVWTOP 342
Db      329 STQGFQWDQPIADNKTKEGRAM-----NRRVFATITGSRITVVVQP 368

RESULT 64
ADF29221
ID      ADF29221 standard; protein; 272 AA.
XX
AC      ADF29221;
XX
DT      12-FEB-2004 (first entry)
XX
DE      Bacterial virulence associated Pasteurella multocida protein PM0586.
XX
KW      antibacterial; vaccine; mutant; Gram negative bacterium; mutation;
KW      attenuated virulence; immunogenic composition; passive immunization;
KW      insertion site; transposon tagged mutagenesis.
XX
OS      Pasteurella multocida.
XX
FN      EPI350796-A1.
XX
PD      08-OCT-2003.
XX
PF      05-APR-2002; 2002EP-00290861.
XX
PR      05-APR-2002; 2002EP-00290861.
XX
PA      (MERI-) MERIAL.
XX
PI      Crooke HR, Shea JE, Feldman RG, Coutebroze SG, Le Gros F;
XX
WPI; 2003-781146/74.
DR      N-PSDB; ADF29220.
XX
XX      New attenuated mutant of a Gram-negative bacteria, useful for the
PT      production of immunogenic or vaccine compositions for the prevention of
PT      bacterial infections, particularly Gram negative bacteria.
XX
XX      Example 4; SEQ ID NO 13; 96pp; English.
XX
XX      The invention relates to a mutant Gram negative bacterium (Pasteurella
CC      multocida) comprising a mutation in a nucleotide sequence which codes for
CC      a polypeptide having an identity which is equal or more than 70%, 75%,
CC      80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% with an amino acid sequence
CC      encoded by any of 29 fully defined sequences of 267-2832 bp, given in the
CC      specification, the mutation resulting in attenuated virulence of the
CC      bacterium. The attenuated mutant is useful for the production of
CC      immunogenic or vaccine compositions for the prevention of bacterial
CC      infections, particularly Gram negative bacteria. The antibody preparation
CC      is useful for the production of a passive immunization composition of a
CC      therapeutic composition against Gram-negative bacteria. This sequence
CC      represents the Pasteurella multocida protein PM0773 which is involved in
CC      bacterial virulence.
XX
SQ      Sequence 272 AA;
Query Match      13.3%; Score 242; DB 7; Length 272;
Best Local Similarity 45.9%; Pred. No. 2.3e-13;
Matches 56; Conservative 22; Mismatches 38; Indels 6; Gaps 4;
Qy      213 FTLKSDVLFNPNKATLKPEGOQALDQLYTQLSNMDPKDGSVAVVLGYTDRIGSEAYNQOLS 272
Db      134 FSLSGDPLDFNFKDLSLTAKGKEVVDVSATQKASDAKE--VKVAGFTDRLGSEAYNKLKLS 191
Qy      273 EKRAQSVVDYLVAKGTPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRVEIEV 332
Db      192 QRRADRYKARLIEQGV-AANIHAVGYGKAQOV--KACDDVQG-AALRDLRPNRRRVEITA 247
```

```
Qy      333 KG 334
Db      248 SG 249

RESULT 65
ADG32432
ID  ADG32432 standard; protein; 272 AA.
XX
AC  ADG32432;
XX
DT  26-FEB-2004 (first entry)
XX
DE  Pasteurella multocida PM0586 protein, a homologue of PM70 SeqID 13.
XX
KW  immunogenic; vaccine; bacterial infection; Pasteurellaceae; immunogen;
KW  allergen; growth factor; cytokine; antibacterial;
KW  transposon insertion site; attenuated gram negative bacteria.
XX
OS  Pasteurella multocida.
XX
PN  WO2003086277-A2.
XX
PD  23-OCT-2003.
XX
PF  04-APR-2003; 2003WO-US010308.
XX
PR  05-APR-2002; 2002US-0370282P.
PR  03-APR-2003; 2003US-00406686.
XX
PA  (MERI-) MERIAL LLC.
XX
PI  Crooke HR, Shea JE, Feldman RG, Coutebroze SG, Legros F;
XX
DR  WPI; 2003-845250/78.
DR  N-PSDB; ADG32431.
XX
PT  New mutant gram negative bacterium having attenuated virulence, useful
PT  for preparing a composition or vaccine for preventing bacterial
PT  infections.
XX
PS  Example 4; SEQ ID NO 13; 170pp; English.
XX
CC  This invention relates to novel live attenuated gram negative bacteria
CC  useful for immunogenic compositions and in vaccines to prevent bacterial
CC  infections. Specifically, it refers to a mutant gram negative bacterium
CC  from the Pasteurellaceae family, having a mutation in a first nucleotide
CC  sequence that codes for a first polypeptide, and results in the bacterium
CC  having attenuated virulence. This mutation can be a deletion, insertion
CC  or replacement of nucleic acids in a regulatory element or coding
CC  sequence of a gene that encodes an immunogen such as a viral, parasitic
CC  or bacterial agent, allergen, growth factor, therapeutic protein or
CC  cytokine. The present invention describes a method for attenuating live
CC  bacteria that reduces or abolishes pathogenicity, decreases bacterial
CC  growth rate and thereby prevents cell death. Accordingly, these
CC  compositions have antibacterial activity and can be administered in an
CC  antibody preparation. This polypeptide sequence is a homologue of the
CC  Pasteurella multocida PM70 protein that is disrupted by insertion of a
CC  transposon to generate a mutant of the invention.
XX
SQ  Sequence 272 AA;

Query Match      13.3%; Score 242; DB 7; Length 272;
Best Local Similarity 45.9%; Pred. No. 2.3e-13;
Matches 56; Conservative 22; Mismatches 38; Indels 6; Gaps 4;

Qy      213 FTLKSDVLFNFNKATLKEPGQALDVLQTSNMDPKDGSVAVLGYTDRIIGSEAYNQOLS 272
Db      134 FLSLSDFLFDNFKSLTAKGEVDVSVAQLKASDAKE--VKVAGFTDRLGSEAYNLKLS 191

Qy      273 EKRAQSVVDYILVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 332
Db      192 QRRADRVKARLIEQGV--AANIHAVGYGKAQV--KACDDVQG--AALRDLCLPNNRRVEITA 247

Qy      333 KG 334
Db      248 SG 249

RESULT 66
ADM94951
ID  ADM94951 standard; protein; 370 AA.
XX
AC  ADM94951;
XX
DT  17-JUN-2004 (first entry)
XX
DE  OprF-CBD fusion protein SEQ ID NO:22.
XX
KW  major outer membrane protein; OprF; fusion protein;
KW  cellulose binding domain; cell surface polypeptide; plant growth;
KW  plant health; CBD.
XX
OS  Hypocrea jecorina.
OS  Asospirillum brasiliense.
OS  Chimeric.
XX
PN  GB2389584-A.
XX
PD  17-DEC-2003.
XX
PF  14-JUN-2002; 2002GB-00013760.
XX
PR  14-JUN-2002; 2002GB-00013760.
XX
PA  (NHYD ) NORSK HYDRO AS.
XX
PI  Vande Broek A, Van Boxel N, Vanderleyden J, Goddard P;
PI  Srinivasan M;
XX
DR  WPI; 2004-055505/06.
DR  N-PSDB; ADM94950.
XX
PT  Fusion protein comprising a cellulose binding domain peptide, and cell
PT  surface polypeptide capable of causing the cellulose binding domain
PT  peptide to be exposed on surface of cell, useful for improving plant
PT  growth.
XX
PS  Claim 7; SEQ ID NO 22; 92pp; English.
XX
CC  The invention relates to a novel fusion protein (I) comprising a
CC  cellulose binding domain peptide, and a cell surface polypeptide capable
CC  of causing the cellulose binding domain peptide to be exposed on the
CC  surface of a cell. A cell transformed with a nucleic acid encoding a
CC  cellulase binding domain peptide is useful for improving plant growth or
CC  health, prophylactically or otherwise by applying the cell to the roots
CC  of a plant. The present sequence represents a fusion protein of the
CC  invention.
XX
SQ  Sequence 370 AA;

Query Match      13.2%; Score 240.5; DB 8; Length 370;
Best Local Similarity 29.0%; Pred. No. 4.9e-13;
Matches 95; Conservative 39; Mismatches 123; Indels 71; Gaps 15;

Qy      34 GNGFQNNNGPTRN--DOLGAGAFGGYGV-----NPVLGEMGVDMIGRMAYKGSV 81
Db      82 GTGRPLNGITQSHYGCGGIGYSGPTVCASGTTCCQVLNPPYS-----QCLGRPKIGDGT 136

Qy      82 DNGAFKAQGVQLTAK--LGYPITDLDIYTRLGMVWRADSKGNVASTGVSRSEHDTGVS 139
Db      137 SS-----LTAQYHFGQAGVDSLAPYVE--GG--FGHQSRGNVKADG--HSGRDQSTL 182

Qy      140 PVFAGGVEMAVTRDIATRLLEYQWVNNTIGDAGTGVTRP--DNG-----MLSLGVGYRRGOE 192
Db      183 AIAGAGVKYFTNNVYAR-----AGVEADYALDNGKWDYSALVGLGVN--FGGN 229
```


Db 114 AGLAHQNIITNINSDSQGQMTMANIGLKYFTENFFAKASLDGQVGL--EKRDNGHQ 171
Qy 180 ---MLSLGVSVRFGQEDAPVVPAPAPAPAPAVAT----- 210
Db 172 GEMWAGLGVGFGSKA----APAPVADVCSDDNDGVDKCPDTPANVTVDAN 227
Qy 211 -----KHFTLKSDVLFNFNKATLKPEGQALDQLYTQLSNM-----DPKDGSAVILGYT 259
Db 228 GCPAFAEVRVQLDVKFDFKSKVK-----ENSYADIKNLADFMKQYPTSTTVEGHT 280
Qy 260 DRIGSEAYNQOLSEKRAQSVVDYLVAK-GIPAGKISARGMGESNPVTGNTCDNVKARAAL 318
Db 281 DSVGTDAYNQKLSERRANAVRDVLVNEYGVGGRVNAVGYGESRPV----ADNATAEGRA 336
Qy 319 IDCLAPDRRVEIEVK 333
Db 337 I-----NRRVEAEVE 346

RESULT 69
ABO81348
ID ABO81348 standard; protein; 351 AA.
AC ABO81348;
XX
XX 29-JUL-2004 (first entry)
XX
XX Pseudomonas aeruginosa polypeptide #13523.
DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
KW Pseudomonas aeruginosa.
OS
FN US5551795-B1.
XX
XX 22-APR-2003.
XX
XX 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
PI WPI; 2003-615309/58.
XX
DR N-ESDB; ABD14919.
XX

Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 30094; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX

SQ Sequence 351 AA;
Query Match 12.7%; Score 231.5; DB 7; Length 351;
Best Local Similarity 26.0%; Pred. No. 3e-12;
Matches 82; Conservative 43; Mismatches 87; Indels 103; Gaps 14;
Qy 97 LGVPIITDLDIYTRLGQWVRADSKGNVAS-----TCVSRSEH-----DTGVSPVFA 143
Db 58 IGYFLTDDVELALSYGVEY---HDVRGYETCNKKVHGNLTSLDAIYHFGTPGVLRPVVS 114
Qy 144 GGV-----EWAVTRDIATRIEYQMVNNI-----GDAGTVGTTPDNG-- 179
Db 115 AGLAHQNIITNINSDSQGQMTMANIGLKYFTENFFAKASLDGQVGL--EKRDNGHQ 172
Qy 180 ---MLSLGVSVRFGQEDAPVVPAPAPAPAPAVAT----- 210
Db 172 GEMWAGLGVGFGSKA----APAPVADVCSDDNDGVDKCPDTPANVTVDAN 228
Qy 211 -----KHFTLKSDVLFNFNKATLKPEGQALDQLYTQLSNM-----DPKDGSAVILGYT 259
Db 229 GCPAFAEVRVQLDVKFDFKSKVK-----ENSYADIKNLADFMKQYPTSTTVEGHT 281
Qy 260 DRIGSEAYNQOLSEKRAQSVVDYLVAK-GIPAGKISARGMGESNPVTGNTCDNVKARAAL 318
Db 282 DSVGTDAYNQKLSERRANAVRDVLVNEYGVGGRVNAVGYGESRPV----ADNATAEGRA 337
Qy 319 IDCLAPDRRVEIEVK 333
Db 338 I-----NRRVEAEVE 347
RESULT 70
ADM46159
ID ADM46159 standard; protein; 349 AA.
XX
XX ADM46159;
XX
XX 17-JUN-2004 (first entry)
XX
XX Acinetobacter outer membrane protein A (OMP A).
DE Outer membrane protein A; OMP A; IL-8; interleukin-8; peptic ulcer;
KW cancer; respiratory disease; sepsis; antiulcer; cytostatic;
KW antibacterial; immunosuppressive.
XX
XX Acinetobacter sp.
XX
XX Key Location/Qualifiers
FH 22. .349
DR Region /note= "Specifically claimed in Claim 9"
XX
XX FT Peptide 36. .45
XX /note= "Antigenic peptide. Specifically claimed in Claim
XX 2"
XX FT Peptide 111. .120
XX /note= "Antigenic peptide. Specifically claimed in Claim
XX 2"
XX FT Peptide 129. .147
XX /note= "Antigenic peptide. Specifically claimed in Claim
XX 2"
XX FT Peptide 337. .349
XX /note= "Antigenic peptide. Specifically claimed in Claim
XX 2"
XX US6713062-B1.
XX
XX 30-MAR-2004.
XX
XX 17-MAY-2000; 2000US-00573630.
XX
XX 17-MAY-1999; 99US-0134399P.
XX
XX (UNMI) UNIV MICHIGAN.
XX

PR 23-APR-1998; 98AU-00003128.
PR 05-MAY-1998; 98AU-00003338.
PR 22-MAY-1998; 98AU-00003654.
PR 29-JUL-1998; 98AU-00004917.
PR 30-JUL-1998; 98AU-00004963.
PR 04-AUG-1998; 98AU-00005028.
XX
PA (CSLC-) CSL LTD.
XX
XX Ross BC, Barr IG, Patterson MA, Agius CT, Rothel LJ, Margetts MB;
PI Hocking DM, Webb EA;
XX
XX WPI: 1999-385613/32.
DR N-PSDB; AAX91708.
XX
XX Antigenic Porphyromonas gingivalis peptides for preventing gingivitis.
XX
XX Claim 1; Page 471-472; 588pp; English.
XX
XX AAX91536 to AAX91801 encode two hundred and sixty six antigenic
CC Porphyromonas gingivalis (PG) polypeptide sequences given in AAX34318 to
CC AAX34583. AAX91802 to AAX91989 represent PCR primers used in the
CC isolation of the PG polypeptides. The PG polypeptides have antibacterial
CC activity with a vaccine mechanism of action. The PG polypeptides can be
CC used as vaccines especially against Porphyromonas gingivalis. Probes can
CC be used to detect Porphyromonas gingivalis in standard hybridisation
CC assays. Porphyromonas gingivalis is involved in periodontal disease
CC especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
CC (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 391 AA;
XX
Query Match 9.6%; Score 175.5; DB 2; Length 391;
Best Local Similarity 22.6%; Pred. No. 4.6e-07;
Matches 87; Conservative 55; Mismatches 126; Indels 117; Gaps 18;
Qy 7 LNAAPKONTWYAGGKL-----GWSQVHDTGFGNGFQNNNGPTRNDQLGA- 51
Db 16 LNSAQENTVPATGQLPAKVFARNAKAGSNWFTVLOGGVAAQFLNDNNKDLMDRLGAI 75
Qy 52 -----GAFGGYQVNPYLG---FEMGYD----- 70
Db 76 GSLSVGKTHSPFPATRLQINGGQAHTFLGKNGEQEIINTNFGAAHDFMDFVNVYFAPYRE 135
Qy 71 -----WLGRLMAYKGSVDNGAFKAQGVQ-LTAKLGYPTDLDLDIYTRLGGMV-WRAD5 120
Db 136 NRFFHLIPWVG-VGYQHKFGISEWSKNVESLTANVGWMA-----FRLGKRVDFVIEA 188
Qy 121 KGNVASTGVSRSSEHDTGVSPVF---AG-----GVEWAVTRDIATRL-----EYQW 162
Db 189 QAAHSNLSRA-YNAKKTVPFEDPAGRYNGFGMGATAGLNFRLGAVGFNAIXPMDYAL 247
Qy 163 VNNIGDAGTVGTRPDNGMLSLGVSRYFQOE-----DAAPVAVP-APAPAPEVATKHFTLKS 217
Db 248 INDL-----NGQIN-----RLRSEVEELSKREVSPCEPTEVTPVTKTENILTEK 291
Qy 218 DVLFNFNKA TLKPEGOQALDQLYTQLSNMDPKGSVAVLGYTDRIGSEAYNQQLSEKRAQ 277
Db 292 AVLRFEDSHVV---DKDQILNLYDVAQVFQKTNBPITVVGADPTGNTQYNEKLSERRAK 348
Qy 278 SVVDYLVNAK-GIPAGKISARGHGES 301
Db 349 AVVDVLTKGYGVPSSELSIVENKGD5 373
RESULT 90
AAX34365
ID AAX34365 standard; protein; 395 AA.
XX
XX AAX34365;
XX
XX 27-AUG-2003 (revised)
DT 20-MAR-2003 (revised)

DT 25-AUG-1999 (first entry)
XX Porphyromonas gingivalis protein PG32.
XX
XX Porphyromonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
KW antigenic.
XX
XX Porphyromonas gingivalis.
XX OS
XX PN PN
XX W09929870-A1.
XX
XX 17-JUN-1999.
XX
XX 10-DEC-1998; 98WO-AU001023.
XX
XX 10-DEC-1997; 97AU-00000839.
PR 31-DEC-1997; 97AU-00001182.
PR 30-JAN-1998; 98AU-00001546.
PR 10-MAR-1998; 98AU-00002264.
PR 09-APR-1998; 98AU-00002911.
PR 23-APR-1998; 98AU-00003128.
PR 05-MAY-1998; 98AU-00003338.
PR 22-MAY-1998; 98AU-00003654.
PR 29-JUL-1998; 98AU-00004917.
PR 30-JUL-1998; 98AU-00004963.
PR 04-AUG-1998; 98AU-00005028.
XX
XX (CSLC-) CSL LTD.
XX
XX Ross BC, Barr IG, Patterson MA, Agius CT, Rothel LJ, Margetts MB;
PI Hocking DM, Webb EA;
XX
XX WPI: 1999-385613/32.
DR N-PSDB; AAX91583.
XX
XX Antigenic Porphyromonas gingivalis peptides for preventing gingivitis.
XX
XX Claim 1; Page 327-328; 588pp; English.
XX
XX AAX91536 to AAX91801 encode two hundred and sixty six antigenic
CC Porphyromonas gingivalis (PG) polypeptide sequences given in AAX34318 to
CC AAX34583. AAX91802 to AAX91989 represent PCR primers used in the
CC isolation of the PG polypeptides. The PG polypeptides have antibacterial
CC activity with a vaccine mechanism of action. The PG polypeptides can be
CC used as vaccines especially against Porphyromonas gingivalis. Probes can
CC be used to detect Porphyromonas gingivalis in standard hybridisation
CC assays. Porphyromonas gingivalis is involved in periodontal disease
CC especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
CC (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 395 AA;
XX
Query Match 9.6%; Score 175.5; DB 2; Length 395;
Best Local Similarity 22.6%; Pred. No. 4.6e-07;
Matches 87; Conservative 55; Mismatches 126; Indels 117; Gaps 18;
Qy 7 LNAAPKONTWYAGGKL-----GWSQVHDTGFGNGFQNNNGPTRNDQLGA- 51
Db 20 LNSAQENTVPATGQLPAKVFARNAKAGSNWFTVLOGGVAAQFLNDNNKDLMDRLGAI 79
Qy 52 -----GAFGGYQVNPYLG---FEMGYD----- 70
Db 80 GSLSVGKTHSPFPATRLQINGGQAHTFLGKNGEQEIINTNFGAAHDFMDFVNVYFAPYRE 139
Qy 71 -----WLGRLMAYKGSVDNGAFKAQGVQ-LTAKLGYPTDLDLDIYTRLGGMV-WRAD5 120
Db 140 NRFFHLIPWVG-VGYQHKFGISEWSKNVESLTANVGWMA-----FRLGKRVDFVIEA 192
Qy 121 KGNVASTGVSRSSEHDTGVSPVF---AG-----GVEWAVTRDIATRL-----EYQW 162
Db 193 QAAHSNLSRA-YNAKKTVPFEDPAGRYNGFGMGATAGLNFRLGAVGFNAIXPMDYAL 251
Qy 163 VNNIGDAGTVGTRPDNGMLSLGVSRYFQOE-----DAAPVAVP-APAPAPEVATKHFTLKS 217

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Db 296 AVLFRFDHVV---DKDQLINLYDVAQPVKETNEPITVGVADPTGNTQYNEKLSERRAK 352
Qy 278 SVDYLYLAK-CIPAGKISARGMGES 301
Db 353 AVVDVLTKGYVPSBELISVEWKGDS 377

RESULT 91
ABO67212
ID ABO67212 standard; protein; 633 AA.
XX AC ABO67212;
XX DT 29-JUL-2004 (first entry)
XX DE Klebsiella pneumoniae polypeptide seqid 13729.
XX KW Recombinant expression vector; transcription regulatory element;
XX KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX OS Klebsiella pneumoniae.
XX PN US6610836-B1.
XX PD 26-AUG-2003.
XX PF 27-JAN-2000; 2000US-00489039.
XX PR 29-JAN-1999; 99US-0117747P.
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Breton GL, Osborne M;
XX WPI; 2003-895346/82.
XX N-PSDB; ABD00783.
XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
XX preparing a vaccine composition against Klebsiella pneumoniae.
XX Disclosure; SEQ ID NO 13729; 932pp; English.
XX The invention describes a new isolated nucleic acid encoding a Klebsiella
XX pneumoniae polypeptide. Also described are: a recombinant expression
XX vector comprising the nucleic acid, operably linked to a transcription
XX regulatory element; and a cell comprising the recombinant expression
XX vector. The nucleic acid is useful for preparing a vaccine composition
XX against Klebsiella pneumoniae. This is the amino acid sequence of a
XX Klebsiella pneumoniae polypeptide of the invention
XX Sequence 633 AA;
Query Match 9.6%; Score 175; DB 7; Length 633;
Best Local Similarity 33.0%; Pred. No. 1e-06;
Matches 59; Conservative 28; Mismatches 64; Indels 28; Gaps 8;
Qy 168 DAGVTGTPDNM---LSLGSVSYRFGQEDAPVV-----APAPAPEVATKHFTL 215
Db 441 DAALLDSWARNGVPLRLSLGLYH--GEQIRLPLLEAIRGYVPPPPPGFVQHVADPVR 498
Qy 216 KSDVLNFKNATLKPEGQAALDQLYTQLSNMDDPKDG-SAVVLGYTDRIGSEAYNQQLSEK 274
Db 499 DMSLSFDTGKVLKPGSTK---RLVSSLMDIKARPGWLIIVAGHTDSVGEKANQLLSLK 555
Qy 275 RAQSVVDYLYAKG-IPAGKISARGMGESNPVTGNTCDNVKARAALIDCLADPRRVIEV 332
Db 556 RAESVRDMWRDTGDVPDSCFAVQGYGESRPIATN--DTPPEGRAL-----NRRVEISL 605
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RESULT 92
ABU41527
ID ABU41527 standard; protein; 229 AA.
XX AC ABU41527;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #27054.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Pseudomonas syringae.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
XX N-PSDB; ACA45397.
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 69451; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX required for proliferation in cells other than S. aureus, S. typhimurium,
XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
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Result No.	Score	Query Match	Length	DB	ID	Description
1	1813	99.5	344	14	US-10-169-953-2	Sequence 2, Appli
2	1520	83.4	346	16	US-10-467-421-90	Sequence 90, Appl
3	1520	83.4	346	16	US-10-467-421-90	Sequence 97, Appl
4	1520	83.4	346	18	US-10-946-647-1413	Sequence 1413, Ap
5	1520	83.4	346	18	US-10-946-647-1413	Sequence 1413, Ap
6	1514	83.1	346	18	US-10-946-647-1448	Sequence 1448, Ap
7	1508	82.8	350	18	US-10-946-647-1424	Sequence 1424, Ap
8	1504	82.5	350	18	US-10-946-647-1377	Sequence 1377, Ap
9	1504	82.5	350	18	US-10-946-647-1389	Sequence 1389, Ap
10	1504	82.5	350	18	US-10-946-647-1395	Sequence 1395, Ap
11	754	41.4	190	16	US-10-416-708A-24	Sequence 24, Appl

85	133	7.3	226	14	US-10-156-761-10782	Sequence 10782, A	158	100.5	5.5	482	16	US-10-758-846-92	Sequence 92, Appl
86	133	7.3	380	10	US-09-998-279-26	Sequence 26, Appl	159	100.5	5.5	663	17	US-10-625-972-7	Sequence 7, Appl
87	133	7.3	380	15	US-10-283-024-4	Sequence 4, Appl	160	100	5.5	367	14	US-10-229-567-30	Sequence 30, Appl
88	133	7.3	385	10	US-09-998-279-24	Sequence 24, Appl	161	100	5.5	367	16	US-10-413-501-10	Sequence 10, Appl
89	130.5	7.2	315	18	US-10-450-763-48136	Sequence 48136, A	162	100	5.5	367	17	US-10-723-164-10	Sequence 10, Appl
90	128.5	7.1	316	15	US-10-323-069A-125	Sequence 125, App	163	99	5.4	19	18	US-10-946-647-1189	Sequence 1189, App
91	128.5	7.1	316	17	US-10-851-965-125	Sequence 125, App	164	98.5	5.4	214	16	US-10-467-534-78	Sequence 78, Appl
92	127.5	7.0	323	15	US-10-323-069A-126	Sequence 126, App	165	98.5	5.4	866	15	US-10-282-122A-43305	Sequence 43305, A
93	127.5	7.0	323	17	US-10-851-965-126	Sequence 126, App	166	98.5	5.4	4326	17	US-10-831-070-18	Sequence 18, Appl
94	126.5	6.9	33	18	US-10-920-244A-11	Sequence 11, Appl	167	98	5.4	473	15	US-10-424-599-227005	Sequence 227005, A
95	125.5	6.9	29	18	US-10-920-244A-4	Sequence 4, Appl	168	97.5	5.4	742	17	US-10-732-923-17477	Sequence 17477, A
96	125.5	6.9	29	18	US-10-920-244A-6	Sequence 6, Appl	169	97.5	5.4	1683	9	US-10-450-763-55158	Sequence 55158, A
97	123.5	6.8	2799	15	US-10-282-122A-65564	Sequence 65564, A	170	97	5.3	192	9	US-09-747-348-2	Sequence 2, Appl
98	122	6.7	168	17	US-10-639-387-4	Sequence 4, Appl	171	97	5.3	192	14	US-10-334-137-2	Sequence 2, Appl
99	121.5	6.7	366	15	US-10-323-069A-121	Sequence 121, App	172	97	5.3	192	15	US-10-312-273-37	Sequence 37, Appl
100	121.5	6.7	366	17	US-10-851-965-121	Sequence 121, App	173	97	5.3	192	15	US-10-289-762-830	Sequence 830, App
101	120.5	6.6	29	18	US-10-920-244A-7	Sequence 7, Appl	174	97	5.3	192	20	US-11-070-478-2	Sequence 2, Appl
102	120.5	6.6	350	16	US-10-474-792-166	Sequence 166, App	175	97	5.3	481	16	US-10-758-846-93	Sequence 93, Appl
103	120	6.6	153	16	US-10-467-421-23	Sequence 23, Appl	176	97	5.3	1083	18	US-10-450-763-56070	Sequence 56070, A
104	120	6.6	153	16	US-10-467-421-25	Sequence 25, Appl	177	96.5	5.3	188	17	US-10-498-327-173	Sequence 173, App
105	119.5	6.6	29	18	US-10-920-244A-5	Sequence 5, Appl	178	96.5	5.3	427	18	US-10-946-647-1374	Sequence 1374, App
106	117.5	6.4	29	18	US-10-920-244A-8	Sequence 8, Appl	179	96.5	5.3	452	15	US-10-282-122A-75165	Sequence 75165, A
107	117.5	6.4	344	15	US-10-451-337-6	Sequence 6, Appl	180	96	5.3	847	15	US-10-282-122A-59134	Sequence 59134, A
108	117	6.4	330	15	US-10-451-337-12	Sequence 12, Appl	181	96	5.3	901	16	US-10-437-963-184559	Sequence 184559, A
109	117	6.4	330	15	US-10-451-337-11	Sequence 11, Appl	182	95.5	5.2	468	15	US-10-425-114-66751	Sequence 66751, A
110	117	6.4	330	15	US-10-451-337-16	Sequence 16, Appl	183	95	5.2	366	15	US-10-282-122A-45735	Sequence 45735, A
111	117	6.4	330	15	US-10-451-337-39	Sequence 39, Appl	184	95	5.2	367	18	US-10-946-647-1412	Sequence 1412, App
112	117	6.4	330	15	US-10-451-337-40	Sequence 40, Appl	185	95	5.2	429	15	US-10-282-122A-66761	Sequence 66761, A
113	117	6.4	330	15	US-10-451-337-41	Sequence 41, Appl	186	95	5.2	873	15	US-10-282-122A-51068	Sequence 51068, A
114	117	6.4	330	15	US-10-451-337-42	Sequence 42, Appl	187	94.5	5.2	628	16	US-10-425-115-233571	Sequence 233571, A
115	115.5	6.3	29	18	US-10-920-244A-9	Sequence 9, Appl	188	94.5	5.2	908	16	US-10-437-963-161711	Sequence 161711, A
116	115.5	6.3	29	18	US-10-920-244A-10	Sequence 10, Appl	189	94.5	5.2	3896	15	US-10-461-194-133	Sequence 133, App
117	115	6.3	35	18	US-10-946-647-578	Sequence 578, App	190	94	5.2	417	9	US-09-815-242-10254	Sequence 10254, A
118	114.5	6.3	171	17	US-10-639-387-3	Sequence 3, Appl	191	94	5.2	417	15	US-10-282-122A-56641	Sequence 56641, A
119	113	6.2	24	18	US-10-946-647-195	Sequence 195, App	192	94	5.2	536	14	US-10-156-761-81170	Sequence 81170, App
120	113	6.2	24	18	US-10-946-647-438	Sequence 438, App	193	94	5.2	540	15	US-10-424-599-169281	Sequence 169281, A
121	113	6.2	24	18	US-10-946-647-576	Sequence 576, App	194	94	5.2	658	15	US-10-335-977-9518	Sequence 9518, App
122	113	6.2	24	18	US-10-946-647-714	Sequence 714, App	195	94	5.2	680	14	US-10-156-761-8989	Sequence 8989, App
123	111.5	6.1	699	15	US-10-369-493-15453	Sequence 15453, A	196	94	5.2	996	15	US-10-335-977-9519	Sequence 9519, App
124	110	6.0	24	18	US-10-946-647-869	Sequence 869, App	197	94	5.2	1165	11	US-09-837-961-4	Sequence 4, Appl
125	110	6.0	24	18	US-10-946-647-1014	Sequence 1014, App	198	94	5.2	1165	16	US-10-809-953-6	Sequence 6, Appl
126	110	6.0	24	18	US-10-946-647-1170	Sequence 1170, App	199	94	5.2	1165	16	US-10-825-751-4	Sequence 4, Appl
127	110	6.0	30	18	US-10-920-244A-12	Sequence 12, Appl	200	94	5.2	2013	17	US-10-872-874-2	Sequence 2, Appl
128	109.5	6.0	173	17	US-10-639-387-2	Sequence 2, Appl	201	94	5.2	2399	15	US-10-282-122A-59054	Sequence 59054, A
129	109	6.0	225	18	US-10-946-647-1171	Sequence 1171, App	202	93.5	5.1	414	15	US-10-282-122A-48141	Sequence 48141, A
130	109	6.0	195	15	US-10-376-397A-34	Sequence 34, Appl	203	93.5	5.1	417	15	US-10-282-122A-48141	Sequence 48141, A
131	109	6.0	195	17	US-10-889-527-34	Sequence 34, Appl	204	93.5	5.1	551	15	US-10-282-122A-69129	Sequence 69129, A
132	108	5.9	25	18	US-10-946-647-194	Sequence 194, App	205	93.5	5.1	570	16	US-10-425-114-39389	Sequence 39389, A
133	108	5.9	25	18	US-10-946-647-437	Sequence 437, App	206	93	5.1	196	15	US-10-425-115-302083	Sequence 302083, A
134	108	5.9	25	18	US-10-946-647-574	Sequence 574, App	207	93	5.1	391	16	US-10-174-695-4	Sequence 4, Appl
135	108	5.9	25	18	US-10-946-647-713	Sequence 713, App	208	93	5.1	417	15	US-10-425-115-326360	Sequence 326360, A
136	108	5.9	25	18	US-10-946-647-871	Sequence 871, App	209	93	5.1	417	9	US-10-282-122A-75788	Sequence 1792, A
137	107	5.9	25	18	US-10-946-647-173	Sequence 173, App	210	93	5.1	831	16	US-10-437-963-144353	Sequence 144353, A
138	107	5.9	25	18	US-10-946-647-575	Sequence 575, App	211	93	5.1	998	15	US-10-282-122A-50795	Sequence 50795, A
139	107	5.9	25	18	US-10-946-647-870	Sequence 870, App	212	92.5	5.1	368	15	US-10-424-599-257309	Sequence 257309, A
140	106.5	5.8	195	15	US-10-415-554-4	Sequence 4, Appl	213	92.5	5.1	402	16	US-10-437-963-150861	Sequence 150861, A
141	106.5	5.8	218	15	US-10-415-554-2	Sequence 2, Appl	214	92.5	5.1	642	16	US-10-437-963-151492	Sequence 151492, A
142	106	5.8	23	18	US-10-946-647-193	Sequence 193, App	215	92	5.0	500	16	US-10-437-963-164206	Sequence 164206, A
143	106	5.8	23	18	US-10-946-647-436	Sequence 436, App	216	92	5.0	605	17	US-10-200-545-77	Sequence 17, Appl
144	106	5.8	23	18	US-10-946-647-573	Sequence 573, App	217	92	5.0	2457	15	US-10-282-122A-49854	Sequence 49854, A
145	106	5.8	23	18	US-10-946-647-712	Sequence 712, App	218	92	5.0	3868	15	US-10-461-194-103	Sequence 103, App
146	105.5	5.8	155	17	US-10-639-387-5	Sequence 5, Appl	219	91.5	5.0	366	18	US-10-946-647-1422	Sequence 1422, App
147	105.5	5.8	173	16	US-10-467-421-93	Sequence 93, Appl	220	91.5	5.0	368	18	US-10-994-726-342	Sequence 342, App
148	105.5	5.8	173	16	US-10-467-421-98	Sequence 98, Appl	221	91.5	5.0	488	14	US-10-994-726-341	Sequence 341, App
149	105.5	5.8	781	14	US-10-156-761-12689	Sequence 12689, A	222	91.5	5.0	488	14	US-10-080-170-4	Sequence 4, Appl
150	104	5.7	384	15	US-10-282-122A-59631	Sequence 59631, A	223	91.5	5.0	488	16	US-10-080-170-4	Sequence 4, Appl
151	103	5.7	1074	18	US-10-450-763-55007	Sequence 55007, A	224	91.5	5.0	488	16	US-10-468-356-4	Sequence 4, Appl
152	103	5.7	1325	9	US-09-741-669-304	Sequence 304, App	225	91.5	5.0	673	16	US-10-425-115-320447	Sequence 320447, A
153	102	5.6	23	18	US-10-946-647-868	Sequence 868, App	226	91.5	5.0	879	15	US-10-369-493-10542	Sequence 10542, A
154	102	5.6	23	18	US-10-946-647-1169	Sequence 1013, App	227	91.5	5.0	1238	15	US-10-282-122A-58749	Sequence 58749, A
155	102	5.6	23	18	US-10-946-647-1169	Sequence 1169, App	228	91.5	5.0	1741	9	US-09-971-536-68	Sequence 68, Appl
156	102	5.6	23	18	US-10-946-647-1191	Sequence 1191, App	229	91	5.0	326	15	US-10-354-437-84	Sequence 84, Appl
157	101.5	5.6	1510	15	US-10-418-861B-55	Sequence 55, Appl	230	91	5.0	417	15	US-10-282-122A-60174	Sequence 60174, A

91	5.0	566	16	US-10-437-963-16356
91	5.0	578	17	US-10-732-923-13824
91	5.0	597	9	US-09-793-306-146
91	5.0	609	16	US-10-437-963-128340
91	5.0	705	15	US-10-282-122A-61846
91	5.0	1721	15	US-10-282-122A-62548
91	5.0	2204	15	US-10-282-122A-64364
90.5	5.0	420	15	US-10-282-122A-73414
90.5	5.0	435	15	US-10-282-122A-68116
90.5	5.0	452	15	US-10-282-122A-75764
90.5	5.0	492	15	US-10-425-114-67318
90.5	5.0	834	15	US-10-282-122A-56247
90.5	5.0	978	15	US-10-282-122A-75356
90.5	5.0	1895	15	US-10-369-493-428
90.5	5.0	4620	15	US-10-282-122A-68921
90.5	5.0	7068	16	US-10-203-295-20
90.5	5.0	9477	16	US-10-203-295-37
90	4.9	419	15	US-10-282-122A-55746
90	4.9	440	15	US-10-282-122A-59591
90	4.9	2130	16	US-10-408-765A-2226
89.5	4.9	237	14	US-10-010-160-12
89.5	4.9	863	15	US-10-282-122A-76063
89.5	4.9	4511	15	US-10-429-148B-2
89	4.9	388	16	US-10-437-963-117151
89	4.9	435	15	US-10-282-122A-56258
89	4.9	437	15	US-10-424-599-232588
89	4.9	455	15	US-10-425-114-45559
89	4.9	608	16	US-10-425-115-293005
88.5	4.9	386	9	US-09-741-154-4
88.5	4.9	386	14	US-10-187-900-4
88.5	4.9	392	18	US-10-788-346-7
88.5	4.9	393	17	US-10-674-433-2
88.5	4.9	415	15	US-09-741-154-2
88.5	4.9	415	14	US-10-187-900-2
88.5	4.9	420	9	US-09-905-176-25
88.5	4.9	430	18	US-10-450-763-46590
88.5	4.9	442	16	US-10-733-435-12
88.5	4.9	478	15	US-10-369-493-15486
88.5	4.9	478	15	US-10-369-493-15857
88.5	4.9	492	15	US-10-369-493-16232
88.5	4.9	498	17	US-10-732-923-23926
88.5	4.9	501	16	US-10-793-435-4
88.5	4.9	507	9	US-09-977-260-2
88.5	4.9	507	10	US-09-977-261-2
88.5	4.9	524	16	US-10-425-115-256418
88.5	4.9	567	9	US-09-344-882-30
88.5	4.9	567	14	US-10-293-865-30
88.5	4.9	614	16	US-10-793-435-6
88.5	4.9	624	14	US-10-037-340-159
88.5	4.9	754	16	US-10-793-435-8
88.5	4.9	787	9	US-09-825-294-207
88.5	4.9	787	14	US-09-970-966-207
88.5	4.9	787	14	US-10-212-677-207
88.5	4.9	787	15	US-10-361-811-207
88.5	4.9	787	15	US-10-369-486-207
88.5	4.9	807	9	US-09-825-294-186
88.5	4.9	807	9	US-09-970-966-186
88.5	4.9	807	14	US-10-097-340-306
88.5	4.9	807	14	US-10-212-677-186
88.5	4.9	807	14	US-10-205-194-133
88.5	4.9	807	15	US-10-361-811-186
88.5	4.9	807	15	US-10-369-486-186
88.5	4.9	807	15	US-10-295-027-510
88.5	4.9	807	15	US-10-173-999-6
88.5	4.9	807	16	US-10-793-435-2
88.5	4.9	807	18	US-10-961-139-36
88.5	4.9	835	14	US-10-037-340-310
88.5	4.9	934	14	US-10-037-340-308
88.5	4.9	1082	16	US-10-437-963-198383
88.5	4.9	1273	15	US-10-282-122A-68193

RESULT 1
US-10-169-953-2
; Sequence 2, Application US/10169953
; Publication No. US20030044915A1

Query Match	99.5%	Score 1813;	DB 14;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 5e-160;		
Matches 342;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			

```

RESULT 2
US-10-467-421-90
: Sequence 90, Application US/10467421
: Publication No. US20040116655A1
: GENERAL INFORMATION:
: APPLICANT: Berthet, Francois-Xavier Jacques
: APPLICANT: Denoeil, Philippe
: APPLICANT: Neyt, Cecile Anne
: APPLICANT: Poolman, Jan
: APPLICANT: Thonnard, Joelle
: TITLE OF INVENTION: Vaccine Composition
: FILE REFERENCE: B45259
: CURRENT APPLICATION NUMBER: US/10/467,421
: CURRENT FILING DATE: 2003-08-08
: PRIOR APPLICATION NUMBER: PCT/EP02/01361

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; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103171.5
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 346
; TYPE: PRT
; ORGANISM: E. coli
; US-10-467-421-90

Query Match      83.4%; Score 1520; DB 16; Length 346;
Best Local Similarity 85.0%; Pred. No. 9,8e-133;
Matches 288; Conservative 17; Mismatches 24; Indels 10; Gaps 2;

Qy 6 VLNAAPKDNWTYAGKLGWSQYHDTGTFYNGGFQNNNGPTRNDQLGAGAFGGYQVNPYLG 65
Db 18 VAQAAPKDNWTYTGAKLGWSQYHDTGFI-----NNNGPTHEQLGAGAFGGYQVNPYVGF 72

Qy 66 EMGYDWMGRMAYKGSVDNGAFKAQGVOLTAKLGYPITDDLDIYTRLGGMWVRADSKGNYA 125
Db 73 EMGYDWMGRMPYKGSVENGAFAKAQGVOLTAKLGYPITDDLDIYTRLGGMWVRADTKSN-- 130

Qy 126 STGVSRSSEHDTGVSVPFAGGVEAWVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGV 185
Db 131 ---VYGKNDHTGVSVPFAGGVEYAITPEIATRLLEYQWNNIGDAHTIGTRPDNGMLSLGV 187

Qy 186 SYRFGQEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 245
Db 188 SYRFGQGEAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 247

Qy 246 MDPKDGSAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
Db 248 LDPKDGSAVVLGYTDRIGSDAYNQGLSERRAQSVVDYLVLSKIPADKISARGMGESNPVT 307

Qy 306 GNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTPQQA 344
Db 308 GNTCDNVKQRAALIDCLAPDRRVEIEVKIGIKDVVTPQQA 346

RESULT 3
US-10-467-421-97
; Sequence 97, Application US/10467421
; Publication No. US20040116665A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Denoel, Philippe
; APPLICANT: Neyt, Cecile Anne
; APPLICANT: Poolman, Jan
; APPLICANT: Thonnard, Joelle
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45259
; CURRENT APPLICATION NUMBER: US/10/467,421
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/EP02/01361
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103171.5
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 346
; TYPE: PRT
; ORGANISM: E. coli
; US-10-467-421-97

Query Match      83.4%; Score 1520; DB 16; Length 346;
Best Local Similarity 85.0%; Pred. No. 9,8e-133;
Matches 288; Conservative 17; Mismatches 24; Indels 10; Gaps 2;

Qy 6 VLNAAPKDNWTYAGKLGWSQYHDTGTFYNGGFQNNNGPTRNDQLGAGAFGGYQVNPYLG 65
Db 18 VAQAAPKDNWTYTGAKLGWSQYHDTGFI-----NNNGPTHEQLGAGAFGGYQVNPYVGF 72
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Qy 66 EMGYDWMGRMAYKGSVDNGAFKAQGVOLTAKLGYPITDDLDIYTRLGGMWVRADSKGNYA 125
Db 73 EMGYDWMGRMPYKGSVENGAFAKAQGVOLTAKLGYPITDDLDIYTRLGGMWVRADTKSN-- 130

Qy 126 STGVSRSSEHDTGVSVPFAGGVEAWVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGV 185
Db 131 ---VYGKNDHTGVSVPFAGGVEYAITPEIATRLLEYQWNNIGDAHTIGTRPDNGMLSLGV 187

Qy 186 SYRFGQEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 245
Db 188 SYRFGQGEAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 247

Qy 246 MDPKDGSAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
Db 248 LDPKDGSAVVLGYTDRIGSDAYNQGLSERRAQSVVDYLVLSKIPADKISARGMGESNPVT 307

Qy 306 GNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTPQQA 344
Db 308 GNTCDNVKQRAALIDCLAPDRRVEIEVKIGIKDVVTPQQA 346

RESULT 4
US-10-946-647-1413
; Sequence 1413, Application US/10946647
; Publication No. US20050186217A1
; GENERAL INFORMATION:
; APPLICANT: EMERY, DARYLL A.
; APPLICANT: STRAUB, DARREN E.
; APPLICANT: WONDERLING, LAURA
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
; FILE REFERENCE: 293.00340101
; CURRENT APPLICATION NUMBER: US/10/946,647
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: 60/504,119
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 1448
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1413
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-10-946-647-1413

Query Match      83.4%; Score 1520; DB 18; Length 346;
Best Local Similarity 85.0%; Pred. No. 9,8e-133;
Matches 288; Conservative 17; Mismatches 24; Indels 10; Gaps 2;

Qy 6 VLNAAPKDNWTYAGKLGWSQYHDTGTFYNGGFQNNNGPTRNDQLGAGAFGGYQVNPYLG 65
Db 18 VAQAAPKDNWTYTGAKLGWSQYHDTGFI-----NNNGPTHEQLGAGAFGGYQVNPYVGF 72

Qy 66 EMGYDWMGRMAYKGSVDNGAFKAQGVOLTAKLGYPITDDLDIYTRLGGMWVRADSKGNYA 125
Db 73 EMGYDWMGRMPYKGSVENGAFAKAQGVOLTAKLGYPITDDLDIYTRLGGMWVRADTKSN-- 130

Qy 126 STGVSRSSEHDTGVSVPFAGGVEAWVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGV 185
Db 131 ---VYGKNDHTGVSVPFAGGVEYAITPEIATRLLEYQWNNIGDAHTIGTRPDNGMLSLGV 187

Qy 186 SYRFGQEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 245
Db 188 SYRFGQGEAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 247

Qy 246 MDPKDGSAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
Db 248 LDPKDGSAVVLGYTDRIGSDAYNQGLSERRAQSVVDYLVLSKIPADKISARGMGESNPVT 307

Qy 306 GNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTPQQA 344
Db 308 GNTCDNVKQRAALIDCLAPDRRVEIEVKIGIKDVVTPQQA 346
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; LENGTH: 194
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-416-708A-64

Query Match
Best Local Similarity 41.1%; Score 748; DB 16; Length 194;
Matches 138; Conservative 9; Mismatches 16; Indels 10; Gaps 2;

Qy 6 VLNAAPKONTWYAGKLGWSQVHDTGTFYGNQFNNGPTRNDQLGAGAFGGYQVNPYLGF 65
Db 20 VAQAAPKONTWYTGAKLGWSQVHDTGTFI-----NNNGFTHENQLGAGAFGGYQVNPYVGF 74

Qy 66 EMGYDWMGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRASKGNYA 125
Db 75 EMGYDWMGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN-- 132

Qy 126 STGVSRSEHDTGVSVPFAGGVEMAVTRDIATRLVYQVNNIGDAGTGTGTRPDN 178
Db 133 ---VYGNKHNDGTVSPVFAGGVEMAVTPEIATRLVYQVNNIGDAGTGTGTRPDN 182

RESULT 15
US-10-946-647-1436
; Sequence 1436, Application US/10946647
; Publication No. US20050186217A1
; GENERAL INFORMATION:
; APPLICANT: EMERY, DARYLL A.
; APPLICANT: STRAUB, DARREN E.
; APPLICANT: WONDERLING, LAURA
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
; FILE REFERENCE: 293.00340101
; CURRENT APPLICATION NUMBER: US/10/946,647
; PRIOR FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: 60/504,119
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 1448
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1436
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-946-647-1436

Query Match
Best Local Similarity 39.5%; Score 719.5; DB 18; Length 161;
Matches 137; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

Qy 103 DDLDIYTRLGGMVWRADSKGNVASTGVSRSSEHDTGVSVPFAGGVEMAVTRDIATRLVYQW 162
Db 1 DDLDIYTRLGGMVWRADTKANVPFG-GASYKHDDTGVSPVFAGGVEMAVTPEIATRLVYQW 59

Qy 163 VNNIGDAGTGTGTRPDNGMLSLGVSRYRFGQEDAAPVVAAPAPAPAPAVATKHTFLKSDVLFN 222
Db 60 TNNIGDAHTGTGTRPDNGLLSLGVSRYRFGQGEAAPVVAAPAPAPAPAVQTKHTFLKSDVLFN 119

Qy 223 FNKATLKPEGQALDQLYTQLSNMMDPKDGSVAVLGYTDRIGS 264
Db 120 FNKATLKPEGQALDQLYSLSNLDPKDGSVVVLGYTDRIGS 161

RESULT 16
US-10-432-056-2
; Sequence 2, Application US/10432056
; Publication No. US20040014661A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: HAEUW, Jean-Francois
; APPLICANT: ROBERT, Alain
; TITLE OF INVENTION: PERIPLASMIC DOMAIN OF AN ENTEROBACTERIUM OMP PROTEIN
; FILE REFERENCE: AND ITS USE AS CARRIER OR ADJUVANT
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; FILE REFERENCE: 344 667 - US
; CURRENT APPLICATION NUMBER: US/10/432,056
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 596
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: FR 00/14 909
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-10-432-056-2

Query Match
Best Local Similarity 38.2%; Score 696; DB 15; Length 137;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 208 VATKHFTLKSDVLFNFNFKATLKPEGQALDQLYTQLSNMMDPKDGSVAVLGYTDRIGSEAY 267
Db 1 VATKHFTLKSDVLFNFNFKATLKPEGQALDQLYTQLSNMMDPKDGSVAVLGYTDRIGSEAY 60

Qy 268 NQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRR 327
Db 61 NQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRR 120

Qy 328 VEIEVKGYKEVVTQPOA 344
Db 121 VEIEVKGYKEVVTQPOA 137

RESULT 17
US-10-336-840-9
; Sequence 9, Application US/10336840
; Publication No. US20030219454A1
; GENERAL INFORMATION:
; APPLICANT: TERRY, TAMSIN DEBORAH
; APPLICANT: TSENG, HSING-JU
; APPLICANT: HOBBS, RHONDA IVY
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: DOWNES, JOHN
; TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
; FILE REFERENCE: 37955-0007
; CURRENT APPLICATION NUMBER: US/10/336,840
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/AU01/00822
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Haemophilus paragallinarum
US-10-336-840-9

Query Match
Best Local Similarity 37.8%; Score 689; DB 15; Length 344;
Matches 153; Conservative 46; Mismatches 124; Indels 18; Gaps 7;

Qy 1 MKAI FVLNAAPKONTWYAGKLGWSQVHDTGTFYGNQFNNGPTRNDQLGAGAFGGYQVN 60
Db 13 LTAASVAQAAPQANTFYAGAKAGWASFDGLNQFENSONADGTLRN-SVTYGVFGYQIT 71

Qy 61 PYLGFEMGYDWMGRMAYK-GSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRAD 119
Db 72 DNFAVELGYDDFGRAKLKRGQGETVIKYNTHGAHLSLKASYPVLEGLDYARVGAALIRSD 131

Qy 120 SKGNVASTGVSRSEHDTGVSVPFAGGVEMAVTR--DIATRLVYQVNNIG---DAGTVG 173
Db 132 YKPTKRAAPNQTGTHSHLSKVSVPFAGGLEYNLPSPLEALRVEIYQVWKNVKGVEKDGSRVD 191

Qy 174 TRPDNGMLSLGVSRYRFGQEDAAPVVAAPAPAPAVATKHTFLKSDVLFNFNFKATLKPEGQ 233
```

Db 192 YTPSGSVTAGUSYRFG--SAPV-----EPKVAKTFALNSDVTTFAGKANLRPEAQ 243
Qy 234 QALDQLYTQLSNMDPKGSAAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKI 293
Db 244 NVLDGIYGEIAQL--KSVQVDVAGYTDRIKSEAAKLKLSQRADTVANLYLSKGVQAEVI 301
Qy 294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVK 334
Db 302 SSTGYGEANPVTGAKCDTVKGRKALIACLADRRRVEISVK 342

RESULT 18
US-10-336-840-6
; Sequence 6, Application US/10336840
; Publication No. US20030219454A1
; GENERAL INFORMATION:
; APPLICANT: TERRY, TAMSIN DEBORAH
; APPLICANT: TSENG, HSING-JU
; APPLICANT: HOBBS, RHONDA IVY
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: DOWNES, JOHN
; TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
; FILE REFERENCE: 37955-0007
; CURRENT APPLICATION NUMBER: US/10/336,840
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/AU01/00822
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 344
; TYPE: PRP
; ORGANISM: Haemophilus paragallinarum
US-10-336-840-6
Query Match 37.8%; Score 688; DB 15; Length 344;
Best Local Similarity 44.9%; Pred. No. 3.1e-55;
Matches 153; Conservative 46; Mismatches 124; Indels 18; Gaps 7;
Qy 1 MKAIFVLAAPKONTWYAGKLGWSQYHDTGFGYNGFQNNNGPTRNDOLGAGAFGGYQVN 60
Db 13 LTAASVAQAAPQANTFYAGAKAGWASPHDGLNQFENSQNDAGTLRN-SVTYGVFGYQIT 71
Qy 61 PYLGFEMGYDWMGRMAYK-GSDNGAFKAQGVQVLTAKLYPITDLDIYTRLGGMWRAD 119
Db 72 DNFAVELGYDDFGRAKRQGGETVIKYTHNGAHLKLSKASYPVLEGLDVARVGAALIRSD 131
Qy 120 SKGNYASTGVSRSEHDTGSPVFAAGVEMAVTR--DIATRLLEYQWVNNIG----DAGTVG 173
Db 132 YKPTKRAAPNQTTHSLKSVSPVFAAGLEVNLPSLPALRALRVEYQWVKVGRVEKDGSRVD 191
Qy 174 TRPDNGMLSLGVSYRFGQEDAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 233
Db 192 YTPSGSVTAGUSYRFG--SAPV-----EPKVAKTFALNSDVTTFAGKANLRPEAQ 243
Qy 234 QALDQLYTQLSNMDPKGSAAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKI 293
Db 244 NVLDGIYGEIAQL--KSVQVDVAGYTDRIKSEAAKLKLSQRADTVANLYLSKGVQAEVI 301
Qy 294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVK 334
Db 302 SSTGYGEANPVTGAKCDTVKGRKALIACLADRRRVEISVK 342
RESULT 19
US-09-905-176-22
; Sequence 22, Application US/09905176
; Patent No. US20020150906A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: Debe, Derek A.
; TITLE OF INVENTION: METHOD FOR DETERMINING THREE-DIMENSIONAL PROTEIN STRUCTURE FROM H

; TITLE OF INVENTION: PROTEIN SEQUENCE
; FILE REFERENCE: 265/297
; CURRENT APPLICATION NUMBER: US/09/905,176
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/218,016
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 153
; TYPE: PRP
; ORGANISM: Escherichia coli
US-09-905-176-22
Query Match 37.7%; Score 687; DB 9; Length 153;
Best Local Similarity 79.1%; Pred. No. 1.2e-55;
Matches 129; Conservative 10; Mismatches 14; Indels 10; Gaps 2;
Qy 27 YHDTGFGYNGFQNNNGPTRNDOLGAGAFGGYQVNPYLGFEYDGLGRMAYKSGVDNGAF 86
Db 1 YHDTGLI-----NNGPHTENKLGAGAFGGYQVNPYVGFEMGYDGLGRMPYKGSVENGAY 55
Qy 87 KAQGVQVLTAKLYPITDLDIYTRLGGMWRADSKGNVASTGVSRSEHDTGSPVFAAGV 146
Db 56 KAQGVQVLTAKLYPITDLDIYTRLGGMWRADTSN-----VYGNKHDGTGSPVFAAGV 110
Qy 147 EMAYTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRF 189
Db 111 EYAITPEIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRF 153
RESULT 20
US-10-336-840-3
; Sequence 3, Application US/10336840
; Publication No. US20030219454A1
; GENERAL INFORMATION:
; APPLICANT: TERRY, TAMSIN DEBORAH
; APPLICANT: TSENG, HSING-JU
; APPLICANT: HOBBS, RHONDA IVY
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: DOWNES, JOHN
; TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
; FILE REFERENCE: 37955-0007
; CURRENT APPLICATION NUMBER: US/10/336,840
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/AU01/00822
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 344
; TYPE: PRP
; ORGANISM: Haemophilus paragallinarum
US-10-336-840-3
Query Match 37.6%; Score 685; DB 15; Length 344;
Best Local Similarity 44.9%; Pred. No. 5.8e-55;
Matches 153; Conservative 46; Mismatches 124; Indels 18; Gaps 7;
Qy 1 MKAIFVLAAPKONTWYAGKLGWSQYHDTGFGYNGFQNNNGPTRNDOLGAGAFGGYQVN 60
Db 13 LTAASVAQAAPQANTFYAGAKAGWASPHDGLNQFENSQNDAGTLRN-SVTYGVFGYQIT 71
Qy 61 PYLGFEMGYDWMGRMAYK-GSDNGAFKAQGVQVLTAKLYPITDLDIYTRLGGMWRAD 119
Db 72 DNFAVELGYDDFGRAKRQGGETVIKYTHNGAHLKLSKASYPVLEGLDVARVGAALIRSD 131
Qy 120 SKGNYASTGVSRSEHDTGSPVFAAGVEMAVTR--DIATRLLEYQWVNNIG----DAGTVG 173
Db 132 YKPTKRAAPNQTTHSLKSVSPVFAAGLEVNLPSLPALRALRVEYQWVKVGRVEKDGSRVD 191
Qy 174 TRPDNGMLSLGVSYRFGQEDAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 233


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Db      13  LTAASVAQAAPQANTFYAGAKAGWASFHDGLNQFENSQNAVTLRN-SVTYGVFGYQIT 71
Qy      61  PYLGFEMGYDMLGRMAYKGSVDN-GAFKAQGVQLTAKLGYPITDDLDIYTRLGGVMWRAD 119
Db      72  DNFAVELGYDDFGRAKLRQDGETVKGHTNHGAHLSLKASYPVLEGLDVIYARVGAALIRSD 131
Qy     120  SKGNVASTGVSRSEHDTGVSPVFAGGVWAVTR--DIATRLYQWVNNIG----DAGTVG 173
Db     132  YKPTKRAAPNETHESLKVSPVFAGGLEYNLPSLPALRVEYQWVNVKVRWEKDGSRVD 191
Qy     174  TRPDNGMLSLGVSYPFGQEDAAPVAPAPAPAPAVATKHTLKSVDLNFNFKATLKPEGQ 233
Db     192  YTPSGVSTAGLSYRFGQ--SAPVV-----EPKVAKTFAALNSDVTFAFGKANLRPEAQ 243
Qy     234  QALDQLYTQLSNMDDPKGSVAVLVGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKI 293
Db     244  NVLDGIYGEIAQL--KSVQVDLAGYTDRIQSEAAANLKSQRADTVANLYLVSKGVAQVEVI 301
Qy     294  SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
Db     302  SSTGYGEANPVTGAKCDVAKGRKALIACTADRRRVEISVKG 342

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RESULT 24

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US-10-336-840-7
; Sequence 7, Application US/10336840
; Publication No. US20030219454A1
; GENERAL INFORMATION:
; APPLICANT: TERRY, TAMSIN DEBORAH
; APPLICANT: TSENG, HSING-JU
; APPLICANT: HOBBS, RHONDA IVY
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: DOWNES, JOHN
; TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
; FILE REFERENCE: 37955-0007
; CURRENT APPLICATION NUMBER: US/10/336,840
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/AU01/00822
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Haemophilus paragallinarum
US-10-336-840-7

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Query Match      37.5%; Score 684; DB 15; Length 344;
Best Local Similarity 44.9%; Pred. No. 7.2e-55;
Matches 153; Conservative 45; Mismatches 125; Indels 18; Gaps 7;

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Qy      1  MKAIFVLNAAPKDNWTYAGKLGWSQYHDTGYGNGFQNNNGPTRNDOLGAGAFGGYQVN 60
Db     13  LTAASVAQAAPQANTFYAGAKAGWASFHDGLNQFENSQNAVDTLRN-SVTYGVFGYQIT 71
Qy     61  PYLGFEMGYDMLGRMAYK--GSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGVMWRAD 119
Db     72  DNFAVELGYDDFGRAKRQGGETVKGHTNHGAHLSLKASYPVLEGLDVIYARVGAALIRSD 131
Qy     120  SKGNVASTGVSRSEHDTGVSPVFAGGVWAVTR--DIATRLYQWVNNIG----DAGTVG 173
Db     132  YKPTKRAAPNETHESLKVSPVFAGGLEYNLPSLPALRVEYQWVNVKVRWEKDGSRVD 191
Qy     174  TRPDNGMLSLGVSYPFGQEDAAPVAPAPAPAPAVATKHTLKSVDLNFNFKATLKPEGQ 233
Db     192  YTPSGVSTAGLSYRFGQ--SAPVV-----EPKVAKTFAALNSDVTFAFGKANLRPEAQ 243
Qy     234  QALDQLYTQLSNMDDPKGSVAVLVGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKI 293
Db     244  NVLDGIYGEIAQL--KSVQVDVAGYTDRIQSEAAANLKSQRADTVANLYLVSKGVAQVEVI 301
Qy     294  SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334

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Db     302  SSTGYGEANPVTGAKCDTVKGRKALIACTADRRRVEISVKG 342

RESULT 25
US-10-336-840-10
; Sequence 10, Application US/10336840
; Publication No. US20030219454A1
; GENERAL INFORMATION:
; APPLICANT: TERRY, TAMSIN DEBORAH
; APPLICANT: TSENG, HSING-JU
; APPLICANT: HOBBS, RHONDA IVY
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: DOWNES, JOHN
; TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
; FILE REFERENCE: 37955-0007
; CURRENT APPLICATION NUMBER: US/10/336,840
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/AU01/00822
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Haemophilus paragallinarum
US-10-336-840-10

```

```

Query Match      37.5%; Score 683; DB 15; Length 344;
Best Local Similarity 44.6%; Pred. No. 9e-55;
Matches 152; Conservative 46; Mismatches 125; Indels 18; Gaps 7;

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Qy      1  MKAIFVLNAAPKDNWTYAGKLGWSQYHDTGYGNGFQNNNGPTRNDOLGAGAFGGYQVN 60
Db     13  LTAASVAQAAPQANTFYAGAKAGWASFHDGLNQFENSQNAVDTLRN-SVTYGVFGYQIT 71
Qy     61  PYLGFEMGYDMLGRMAYKGSVDN-GAFKAQGVQLTAKLGYPITDDLDIYTRLGGVMWRAD 119
Db     72  DNFAVELGYDDFGRAKLRQDGETVKGHTNHGAHLSLKASYPVLEGLDVIYARVGAALIRSD 131
Qy     120  SKGNVASTGVSRSEHDTGVSPVFAGGVWAVTR--DIATRLYQWVNNIG----DAGTVG 173
Db     132  YKPTKRAAPNETHESLKVSPVFAGGLEYNLPSLPALRVEYQWVNVKVRWEKDGSRVD 191
Qy     174  TRPDNGMLSLGVSYPFGQEDAAPVAPAPAPAPAVATKHTLKSVDLNFNFKATLKPEGQ 233
Db     192  YTPSGVSTAGLSYRFGQ--SAPVV-----EPKVAKTFAALNSDVTFAFGKANLRPEAQ 243
Qy     234  QALDQLYTQLSNMDDPKGSVAVLVGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKI 293
Db     244  NVLDGIYGEIAQL--KSVQVDLAGYTDRIQSEAAANLKSQRADTVANLYLVSKGVAQVEVI 301
Qy     294  SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
Db     302  SSTGYGEANPVTGAKCDVAKGRKALIACTADRRRVEISVKG 342

```

RESULT 26

```

US-10-336-840-5
; Sequence 5, Application US/10336840
; Publication No. US20030219454A1
; GENERAL INFORMATION:
; APPLICANT: TERRY, TAMSIN DEBORAH
; APPLICANT: TSENG, HSING-JU
; APPLICANT: HOBBS, RHONDA IVY
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: DOWNES, JOHN
; TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
; FILE REFERENCE: 37955-0007
; CURRENT APPLICATION NUMBER: US/10/336,840
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/AU01/00822
; PRIOR FILING DATE: 2001-07-06

```



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; Publication No. US20030219454A1
;
; GENERAL INFORMATION:
; APPLICANT: TERRY, TAMSIN DEBORAH
; APPLICANT: TSENG, HSING-JU
; APPLICANT: HOBB, RHONDA IVY
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: DOWNES, JOHN
;
; TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
;
; FILE REFERENCE: 37955-0007
; CURRENT APPLICATION NUMBER: US/10/336,840
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/AU01/00822
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Artificial Sequence
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: sequence
;
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)
; OTHER INFORMATION: Variable amino acid, preferably Ala
;
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (53)
; OTHER INFORMATION: Variable amino acid, preferably Tyr
;
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (88)
; OTHER INFORMATION: Variable amino acid
;
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (91)
; OTHER INFORMATION: Variable amino acid, preferably Asp
;
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (96)
; OTHER INFORMATION: Variable amino acid, preferably Ile
;
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (98)
; OTHER INFORMATION: Variable amino acid, preferably His
;
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (142)
; OTHER INFORMATION: Asn, Asp, Glu or Gln
;
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (183)
; OTHER INFORMATION: Variable amino acid
;
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (184)
; OTHER INFORMATION: Variable amino acid, preferably Glu
;
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (185)
; OTHER INFORMATION: Variable amino acid, preferably Lys
;
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (263)
; OTHER INFORMATION: Variable amino acid, preferably Leu
;
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (315)
; OTHER INFORMATION: Variable amino acid, preferably Ala
;
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (343)

```

```
Db 189 AGKASYTLNRMGATDYSDISSVSAGLSYRFQ- GAAPVAAPA-----VETKNFAFSS 241
Qy 218 DVLNFKNATLKPEQQALDQLYTQLSNMDDPKGSVAVLVGYTDRIGSEAYNQQLSEKRAQ 277
Db 242 DVLFAFGKSNLKPAAATALDAMQTEINNAGLSNAAIQVNGYTDRIKGESNKLKLSQRAE 301
Qy 278 SVVDYLVAKGIPAGKISARGMESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKE 337
Db 302 TVANYIVSKGAPAAANVTAVGGEANPVTGATCDKVKGRKALIACLAPDRRVEVVOVQGTKE 361
Qy 338 V 338
Db 362 V 362

RESULT 31
US-10-854-299-151
; Sequence 151, Application US/10854299
; Publication No. US20050003512A1
; GENERAL INFORMATION:
; APPLICANT: Lowery E., David, et al.
; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
; FILE REFERENCE: 28341/00435
; CURRENT APPLICATION NUMBER: US/10/854,299
; CURRENT FILING DATE: 2004-05-26
; PRIOR APPLICATION NUMBER: 60/153,453
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/128,689
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/545,199
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 151
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Actinobacillus pleuropneumoniae
US-10-854-299-151
```

```
Query Match 36.8%; Score 671; DB 17; Length 364;
Best Local Similarity 42.4%; Pred. No. 1.3e-53;
Matches 153; Conservative 54; Mismatches 122; Indels 32; Gaps 10;

Qy 1 MKAIFVLNAAPKDNTWYAGKLGWSQYHDTGFYGNFGQNNNGPTR-----NDQLGAGAPGG 56
Db 11 LSAAAVAQAAPQONTFYAGAKAGWASPHDGIQLDSAKNTDRGTYKGINRNSVTYGVFGG 70
Qy 57 YQV--NPYLGF--EMGYDWLGRM----AYKGSVDNGAFK--AQGVQLTAKLGYPTDLD 106
Db 71 YQILNQDKLGLAAELGYDYFGVRGSEKPNKGADKKTFRHAHAGTATIALKPSYEVLPDLD 130
Qy 107 IYTRLG-GMWVRADSKGNVASTGVSRSEHDTGVSVPFAGGVEAWVTRDIATRLLEYQWVNN 165
Db 131 VYGVKGIALVNNTYKTFNAAQEKVKTTRFQS--SLILGAGVEYAILPELAARVEYQWLNN 188
Qy 166 IGDA-----GTGVTGTPDNQMLSLGVSYPFGQEDAAPVVAAPAPAPAPAEVATKHFTLKS 217
Db 189 AGKASYTLNRMGATDYSDISSVSAGLSYRFQ- GAAPVAAPA-----VETKNFAFSS 241
Qy 218 DVLNFKNATLKPEQQALDQLYTQLSNMDDPKGSVAVLVGYTDRIGSEAYNQQLSEKRAQ 277
Db 242 DVLFAFGKSNLKPAAATALDAMQTEINNAGLSNAAIQVNGYTDRIKGESNKLKLSQRAE 301
Qy 278 SVVDYLVAKGIPAGKISARGMESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKE 337
Db 302 TVANYIVSKGAPAAANVTAVGGEANPVTGATCDKVKGRKALIACLAPDRRVEVVOVQGTKE 361
Qy 338 V 338
Db 362 V 362
```

```
RESULT 32
US-10-770-824-8
; Sequence 8, Application US/10770824
; Publication No. US20040198954A1
; GENERAL INFORMATION:
; APPLICANT: Campos, Manuel
; APPLICANT: Baarsch, Mary Jo
; APPLICANT: Rosey, Everett
; APPLICANT: Ankenbauer, Robert
; APPLICANT: Warren-Stewart, Lynn
; APPLICANT: Suiter, Brian
; APPLICANT: Keach, Robin
; TITLE OF INVENTION: NOVEL PROTEINS FROM ACTINOBACILLUS PLEUROPNUEUMONIAE
; FILE REFERENCE: PC9854A
; CURRENT APPLICATION NUMBER: US/10/770,824
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US/09/418,980
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Actinobacillus pleuropneumoniae
US-10-770-824-8

Query Match 36.6%; Score 667; DB 16; Length 364;
Best Local Similarity 42.1%; Pred. No. 3e-53;
Matches 152; Conservative 54; Mismatches 123; Indels 32; Gaps 10;

Qy 1 MKAIFVLNAAPKDNTWYAGKLGWSQYHDTGFYGNFGQNNNGPTR-----NDQLGAGAPGG 56
Db 11 LSAAAVAQAAPQONTFYAGAKAGWASPHDGIQLDSAKNTDRGTYKGINRNSVTYGVFGG 70
Qy 57 YQV--NPYLGF--EMGYDWLGRM----AYKGSVDNGAFK--AQGVQLTAKLGYPTDLD 106
Db 71 YQILNQDKLGLAAELGYDYFGVRGSEKPNKGADKKTFRHAHAGTATIALKPSYEVLPDLD 130
Qy 107 IYTRLG-GMWVRADSKGNVASTGVSRSEHDTGVSVPFAGGVEAWVTRDIATRLLEYQWVNN 165
Db 131 VYGVKGIALVNNTYKTFNAAQEKVKTTRFQS--SLILGAGVEYAILPELAARVEYQWLNN 188
Qy 166 IGDA-----GTGVTGTPDNQMLSLGVSYPFGQEDAAPVVAAPAPAPAPAEVATKHFTLKS 217
Db 189 AGKASYTLNRMGATDYSDISSVSAGLSYRFQ- GAAPVAAPA-----VETKNFAFSS 241
Qy 218 DVLNFKNATLKPEQQALDQLYTQLSNMDDPKGSVAVLVGYTDRIGSEAYNQQLSEKRAQ 277
Db 242 DVLFAFGKSNLKPAAATALDAMQTEINNAGLSNAAIQVNGYTDRIKGESNKLKLSQRAE 301
Qy 278 SVVDYLVAKGIPAGKISARGMESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKE 337
Db 302 TVANYIVSKGAPAAANVTAVGGEANPVTGATCDKVKGRKALIACLAPDRRVEVVOVQGTKE 361
Qy 338 V 338
Db 362 V 362

RESULT 33
US-10-999-363-45
; Sequence 45, Application US/10999363
; Publication No. US2005009258A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Products Inc
; TITLE OF INVENTION: FUSION PROTEINS COMPRISING CARRIERS THAT CAN INDUCE A
; TITLE OF INVENTION: DUAL IMMUNE RESPONSE
; FILE REFERENCE: PC10202A
; CURRENT APPLICATION NUMBER: US/10/999,363
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: US/09/506,078
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: N/A
```



```
; SEQ ID NO 37
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-336-840-37

Query Match      35.3%; Score 643.5; DB 15; Length 352;
Best Local Similarity 42.5%; Pred. No. 4.4e-51;
Matches 156; Conservative 46; Mismatches 104; Indels 61; Gaps 13;

Qy 1 MKAIFVLNAAPKDNNTWYAGGKLGWSQYHD-----TGFGNGFQNNNGPTRNDQLG 50
Db 13 LAASVAQAAPQENTFYAGVAGQASFDGRLALAREYKVGTHRNSFT-----60

Qy 51 AGAFGGYQV----NPYLGFEMGYDWLGRMAYKGSVDNGAFKAQ-----GVQLTAKLGYPI 102
Db 61 YGVFGGYQILNQNNLGLAVELGYDDFGRA--KGR-EKGKTVVKGHTNHGTHLSLKGSEVL 117

Qy 103 DDLDIYTRLGGMVRADSK--GNVASTGVSRSEHDTG-VSPVFAGGVWAVTRDIATRL 159
Db 118 EGLDVGKAGVALVRSYKLYNENSSTLKLGHEHRRASGLFAVGAFYAVLPALAVRLE 177

Qy 160 YQWVNNIGDAGTV-----GMLSLGVSYRFGQEDDAAPVAVAPAPAPE 207
Db 178 YQWLVTRGK-----YRPODKENTALNPWLGSIAGISYRFGQ-GAAPVVA-----APE 226

Qy 208 VATKHTLKSVDLNFNFKATLKPEGQQAALDQLYTQLSNMDPKDGSAAVVLGYTDRIGSEAY 267
Db 227 VVSKTFLNSDVTFAFGKANLKPOQAATLDSIYGEMSQV--KSAKVAAGVYTRIGSDAF 284

Qy 268 NQQLSEKRAQSVVDYLVAKGIPACKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRR 327
Db 285 NVKLSQERADSVANYFVAKGVAADAISATGYGKANPVTGATCDQVKGKALIACFAPDRR 344

Qy 328 VEIEVKG 334
Db 345 VEIAVNG 351

RESULT 39
US-10-770-824-10
; Sequence 10, Application US/10770824
; Publication No. US20040198954A1
; GENERAL INFORMATION:
; APPLICANT: Campos, Manuel
; APPLICANT: Baarsch, Mary Jo
; APPLICANT: Rosey, Everett
; APPLICANT: Ankenbauer, Robert
; APPLICANT: Warren-Stewart, Lynn
; APPLICANT: Suiter, Brian
; APPLICANT: Keach, Robin
; TITLE OF INVENTION: NOVEL PROTEINS FROM ACTINOBACILLUS PLEUROPNEMONIAE
; FILE REFERENCE: PC9854A
; CURRENT APPLICATION NUMBER: US/10/770,824
; CURRENT FILING DATE: 2004-02-03
; PRIOR FILING DATE: 2004-02-03
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Actinobacillus pleuropneumoniae
US-10-770-824-10

Query Match      35.1%; Score 639.5; DB 16; Length 369;
Best Local Similarity 40.7%; Pred. No. 1.1e-50;
Matches 151; Conservative 60; Mismatches 113; Indels 47; Gaps 11;

Qy 1 MKAIFVLNAAPKDNNTWYAGGKLGWSQYHDTGFCYG-NGFQNNNGPTRNDQ-----L 49
Db 11 LSAAVAQAAPQONTFYAGAKVGQSSPH----HGVNQLKSGHDDRYNDKTRKYGINRNSV 66

Qy 50 GAGAFGGYQV----NPYLGFEMGYDWLGRMAYKGSVDNGAFK-----AQGVQLTAKLGY 100
Db 67 TYGVFGGYQILNQNNFGLATLGLDYDYGVRV--RG--NDGEFRAMKHSAGHNFALKPSYE 122

Qy 101 ITDDLDIYTRLGGMVRADSKGNVASTGVSRSE--HDTGVSPVPFAGGVWAVTRDIATRL 158
Db 123 VLPDLVYGVKGVAVVRNDYKSYGAENTNEPTEKFHKLKASTILGAGVEYAILPELAARV 182

Qy 159 EQWVNNIGDAGTV-----GTR-----PONGMLSLGVSYRFGQEDDAAPVAVAPAPAPE 207
Db 183 EQYVLNKGALNKLALVRSQTQVDVDFQYAPDIHSVTAGLSYRFGQGVAVPVW-----EPE 236

Qy 208 VATKHTLKSVDLNFNFKATLKPEGQQAALDQLYTQLSNMDPKDGSAAVVLGYTDRIGSEAY 267
Db 237 VVTKNFAFSDDLVPDFGKSSLKPAATAALDAANTEIANLGLATPAIQVNGYTRIGKEAS 296

Qy 268 NQQLSEKRAQSVVDYLVAKGIPACKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRR 327
```

[illegible]

```

; NAME/KEY: MOD_RES
; LOCATION: (107)
; OTHER INFORMATION: Variable amino acid, preferably Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (113)
; OTHER INFORMATION: Variable amino acid, preferably Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (116)
; OTHER INFORMATION: Variable amino acid, preferably Glu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (125)
; OTHER INFORMATION: Variable amino acid, preferably Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (126)
; OTHER INFORMATION: Variable amino acid, preferably Arg
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (127)
; OTHER INFORMATION: Variable amino acid, preferably Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (129)
; OTHER INFORMATION: Variable amino acid, preferably Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (132)
; OTHER INFORMATION: Ile or Val
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (138)..(140)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (141)
; OTHER INFORMATION: Variable amino acid, preferably Glu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (142)
; OTHER INFORMATION: Variable amino acid, preferably Asn
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (143)
; OTHER INFORMATION: Variable amino acid, preferably Lys
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (144)
; OTHER INFORMATION: Variable amino acid, preferably Arg
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (145)..(146)
; OTHER INFORMATION: Variable amino acid, preferably Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (147)
; OTHER INFORMATION: Variable amino acid, preferably Lys
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (148)
; OTHER INFORMATION: Variable amino acid, preferably Asn
; FEATURE:

```

Query Match 27.8%; Score 506; DB 15; Length 356;
 Best Local Similarity 37.3%; Pred. No. 2.9e-38;
 Matches 131; Conservative 25; Mismatches 169; Indels 26; Gaps 9;

```

Qy 1 MKAIFVLAAPKDNITWAGKLGWSQYHDTGYGNGFQNNNGPTNDQIGAGAFGGYQV- 59
Db 13 LXAASVAQAAPQXNTFYAGXKAGXASFDGLGXXXXXXXXXXXXXRNST-YGVFGGYQIX 71

```

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Qy 60 ---NPYLGFEMGYDWLGRMAYKGSVDN-GAPKAQGVQLTAKLGYPIITDDLDIYTRLGMV 115
Db 72 XXXXXXAVELGYDDFGRAKRXXTVXKHTNRGHLSLKXSYXVLEGLDVYXXGXAL 131
Qy 116 WRADSK---GNVASTGVSRSEHDTGVPFAGGVEMAVTR--DIATRLGYQWVNNIGDAG 170
Db 132 XRSYIKXXXXXXXXXXXXXXXXXXXXXFXAGXEYXXXXLPELAXREYQWXXVGVXXX 191
Qy 171 TVGT-----RPDNGMLSLGVSRYFGQEDAAPVAPAPAPAPAVATKHFTLKSDVLFNF 223
Db 192 XXXXXXXXXXXXXYPXIGSKXAGXSRYFGQ-XXAPVXX-----XPXVXKTFXLNSDVTFAF 245
Qy 224 NKATLKPEGQALDQLYTQLSNMDPKGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYL 283
Db 246 GKANLXPXAQXXLDXIYGEXXQX--KSXVXXAGYTDRIGSAXXKLSQXRADXVANYX 303
Qy 284 VAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
Db 304 VXKGVAXXXISXGTGXANPVTGAXCDXVKGRKALIIACXAXDRRVEIAXVG 354

```

RESULT 42

```

US-10-467-421-92
; Sequence 92, Application US/10467421
; Publication No. US2004011666SAI
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Denoel, Philippe
; APPLICANT: Neyt, Cecile Anne
; APPLICANT: Poolman, Jan
; APPLICANT: Thonhard, Joelle
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45259
; CURRENT APPLICATION NUMBER: US/10/467,421
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/EP02/01361
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103171.5
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-421-92

```

Query Match 14.4%; Score 262; DB 16; Length 236;
 Best Local Similarity 35.0%; Pred. No. 8.6e-16;
 Matches 69; Conservative 29; Mismatches 67; Indels 32; Gaps 6;

```

Qy 164 NNIGDA--GTVGTRPDNGMLSLGVSRYFGQEDAAPVAPAPAP-----APEVATKHFTL 215
Db 42 NNYGECWKNAYFDRASQGRVECG-----DAVAVEPEPEPAPVAVVEQAFQYDEETISL 93
Qy 216 KSDVLFNFKATLKPEGQALDQLYTQLSNMDPKGSAVVLGYTDRIGSEAYNQQLSEKR 275
Db 94 SAKTLFGFDKDSLRAEAQDNLKVLQAQLSRITNVQ--SVRVEGHTDFMGSEKYNQALSERR 151
Qy 276 AQSVVDVILVAKGIPAGKISARGMGESNPVTGNTC-----DNVKAALIDCLAP 324
Db 152 AYVVANNLVSNGVPASRISAVGLGESQAQMTQVCQAEVAKLGAKAKAKKREALTACTEP 211
Qy 325 DRRVEIEVKGYKEVVTO 341
Db 212 DRRVDVKI---RSIVTR 225

```

RESULT 43

```

US-10-467-421-96
; Sequence 96, Application US/10467421
; Publication No. US2004011666SAI
; GENERAL INFORMATION:

```



```
; FILE REFERENCE: B45259
; CURRENT APPLICATION NUMBER: US/10/467,421
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/EP02/01361
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103171.5
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-467-421-91

Query Match      13.8%; Score 251; DB 16; Length 240;
Best Local Similarity 36.3%; Pred. No. 9.4e-15;
Matches 62; Conservative 27; Mismatches 58; Indels 24; Gaps 4;

Qy 190 GOEADAPVVPAPAPAPVATKH-----FTLKSDFLNFNFKATLKPEGQQAQLDQLYT 241
Db 64 GDAVAAPPEPEPEPAPVVPVVEQAPQYVDEITISAKTLFGFDKSLRAEAQDNLKVLQA 123

Qy 242 QLSNMDPKDGSVAVLYGTRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGES 301
Db 124 RLQGTNIQ--SVRVEGHTDFMGSDKYNQALSERAYVYVANNLVSGVPSRISAVGLGES 181

Qy 302 NPVTGNTCD-----NVKARAALIDCLAPDRRVEIEVKYKEVVTQ 341
Db 182 QAQMTQVCEAEVAKLGAKVSKAKKREALIACIEPDRRDVVKI---RSIVTR 229

RESULT 47
US-10-467-421-95
; Sequence 95, Application US/10467421
; Publication No. US20040118665A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Berthet, Philippe
; APPLICANT: Denoel, Philippe
; APPLICANT: Neyt, Cecile Anne
; APPLICANT: Poolman, Jan
; APPLICANT: Thonnard, Joelle
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45259
; CURRENT APPLICATION NUMBER: US/10/467,421
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/EP02/01361
; PRIOR FILING DATE: 2002-02-08
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-467-421-95

Query Match      13.8%; Score 251; DB 16; Length 240;
Best Local Similarity 36.3%; Pred. No. 9.4e-15;
Matches 62; Conservative 27; Mismatches 58; Indels 24; Gaps 4;

Qy 190 GOEADAPVVPAPAPAPVATKH-----FTLKSDFLNFNFKATLKPEGQQAQLDQLYT 241
Db 64 GDAVAAPPEPEPEPAPVVPVVEQAPQYVDEITISAKTLFGFDKSLRAEAQDNLKVLQA 123

Qy 242 QLSNMDPKDGSVAVLYGTRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGES 301
Db 124 RLQGTNIQ--SVRVEGHTDFMGSDKYNQALSERAYVYVANNLVSGVPSRISAVGLGES 181

Qy 302 NPVTGNTCD-----NVKARAALIDCLAPDRRVEIEVKYKEVVTQ 341
Db 182 QAQMTQVCEAEVAKLGAKVSKAKKREALIACIEPDRRDVVKI---RSIVTR 229

; FILE REFERENCE: B45259
; CURRENT APPLICATION NUMBER: US/10/467,421
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/EP02/01361
; PRIOR FILING DATE: 2002-02-08
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-467-421-91

Query Match      13.8%; Score 251; DB 16; Length 240;
Best Local Similarity 36.3%; Pred. No. 9.4e-15;
Matches 62; Conservative 27; Mismatches 58; Indels 24; Gaps 4;

Qy 190 GOEADAPVVPAPAPAPVATKH-----FTLKSDFLNFNFKATLKPEGQQAQLDQLYT 241
Db 64 GDAVAAPPEPEPEPAPVVPVVEQAPQYVDEITISAKTLFGFDKSLRAEAQDNLKVLQA 123

Qy 242 QLSNMDPKDGSVAVLYGTRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGES 301
Db 124 RLQGTNIQ--SVRVEGHTDFMGSDKYNQALSERAYVYVANNLVSGVPSRISAVGLGES 181

Qy 302 NPVTGNTCD-----NVKARAALIDCLAPDRRVEIEVKYKEVVTQ 341
Db 182 QAQMTQVCEAEVAKLGAKVSKAKKREALIACIEPDRRDVVKI---RSIVTR 229

RESULT 48
US-10-988-943-6
; Sequence 6, Application US/10988943
; Publication No. US20050176085A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE
; TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN
; TITLE OF INVENTION: COMPLEX MIXTURES.
; FILE REFERENCE: Proteomics CU2003-269
; CURRENT APPLICATION NUMBER: US/10/988,943
; CURRENT FILING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Neisseria meningitidis (group B)
US-10-988-943-6

Query Match      13.7%; Score 250; DB 18; Length 242;
Best Local Similarity 32.8%; Pred. No. 1.2e-14;
Matches 64; Conservative 34; Mismatches 75; Indels 22; Gaps 5;

Qy 164 NNIGDA--GTGTRPDNGMLSLGVSYRFQGEDAAPVVPAPAPA----PAPEVATKHFTLKS 217
Db 42 NNYGECWKNAYFDKASQGRVECGDAVAAPPEPEPEPAPVVPVVEQAPQYVDEITISLSA 101

Qy 218 DVLFNFNFKATLKPEGQQAQLDQLYTQLSNMDPKDGSVAVLYGTRIGSEAYNQQLSEKRAQ 277
Db 102 KTLFGFDKSLRAEAQDNLKVLQAQLGQTNIQ--SVRVEGHTDFMGSDKYNQALSERRAY 159

Qy 278 SVVDYLVAKGIPAGKISARGMGESNPVTGNTCD-----NVKARAALIDCLAPDR 326
Db 160 VVANNLVSGVPSRISAVGLGESQAQMTQVCEAEVAKLGAKVSKAKKREALIACIEPDR 219

Qy 327 RVEIEVKYKEVVTQ 341
Db 220 RVDVKI---RSIVTR 231

RESULT 49
US-10-406-686A-13
; Sequence 13, Application US/10406686A
; Publication No. US20040033586A1
; GENERAL INFORMATION:
; APPLICANT: CROOKE, HELEN RACHEL
; APPLICANT: SHEA, JACQUELINE ELIZABETH
; APPLICANT: FELDMAN, ROBERT GRAHAM
; APPLICANT: COUTEBROZE, SYLVAIN GABRIEL
; APPLICANT: LEGROS, FRANCOIS-XAVIER
; TITLE OF INVENTION: ATTENUATED GRAM NEGATIVE BACTERIA
; FILE REFERENCE: 454313-3171.1
; CURRENT APPLICATION NUMBER: US/10/406,686A
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/370,282
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-10-406-686A-13

Query Match      13.3%; Score 242; DB 15; Length 272;
Best Local Similarity 45.9%; Pred. No. 7.7e-14;
Matches 56; Conservative 22; Mismatches 38; Indels 6; Gaps 4;

Qy 213 PTLKSDVLFNFNFKATLKPEGQQAQLDQLYTQLSNMDPKDGSVAVLYGTRIGSEAYNQQLS 272
Db 182 QAQMTQVCEAEVAKLGAKVSKAKKREALIACIEPDRRDVVKI---RSIVTR 229
```

Db 134 FSLSGDLFDENKDSLTAKGKEVVDVSVATQLKASDAKE--VKVAGFTDRLGSEAYNLKLS 191
Qy 273 EKRAQSVVDYLVAKIPAGKISARGMGESNPVTGNTCDNVKARAALDCLAPDRRVEIEV 332
Db 192 QRRADRVKARLIEQGV--AANHAVGYKRAQGV--KACDDVOG--AALRDCLRPNRVEITA 247
Qy 333 KG 334
Db 248 SG 249

RESULT 50
US-10-920-244A-13
; Sequence 13, Application US/10920244A
; Publication No. US20050196406A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of California
; APPLICANT: DAUGHERTY, Patrick S.
; APPLICANT: BESSETTE, Paul H.
; APPLICANT: RICE, Jeffrey
; TITLE OF INVENTION: Polypeptide Display Libraries and Methods of Making and Using
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 034044.034
; CURRENT APPLICATION NUMBER: US/10/920,244A
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: US 60/495,698
; PRIOR FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-10-920-244A-13

Query Match 10.5%; Score 191; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 KLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGA 53
Db 2 KLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGA 34

RESULT 51
US-10-389-647-584
; Sequence 584, Application US/10389647
; Publication No. US20040033549A1
; GENERAL INFORMATION:
; APPLICANT: GREENBERG, E. Peter
; APPLICANT: SCHUSTER, Martin
; APPLICANT: LOSTROH, Candl
; TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
; FILE REFERENCE: U12-038CP
; CURRENT APPLICATION NUMBER: US/10/389,647
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 09/653730
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/153022
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 710
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 584
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-389-647-584

Query Match 9.7%; Score 176.5; DB 15; Length 261;
Best Local Similarity 36.5%; Pred. No. 9.2e-08;
Matches 42; Conservative 23; Mismatches 39; Indels 11; Gaps 3;

Qy 218 DVLNFKATLKPEQQALDQLYTQLSNMDPKGSAAVLGYTDRIGSEAYNQQLSEKRAQ 277

Db 143 DVLFDLKDSDLKPGAMENIQQL-AEFLQQNP-BEQVIVEGYTDTSGSANTYNQRLSERRAD 200
Qy 278 SVVDYLVAKIPAGKISARGMGESNPVTGNTCDNVKARAALDCLAPDRRVEIEV 332
Db 201 SVRMALLSRGTSIPRVATRGYKEYPVVASNGTSSGRAM-----NRRVEVTI 246

RESULT 52
US-10-283-024-3
; Sequence 3, Application US/10283024
; Publication No. US20030215402A1
; GENERAL INFORMATION:
; APPLICANT: BARR, Ian G.
; APPLICANT: CZAJKOWSKI, Larissa
; APPLICANT: ROSS, Bruce C.
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS RECOMBINANT
; TITLE OF INVENTION: PROTEINS AND TRUNCATIONS
; FILE REFERENCE: 529282000800
; CURRENT APPLICATION NUMBER: US/10/283,024
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/AU01/00482
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: AU PQ 7182
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-283-024-3

Query Match 9.7%; Score 176; DB 15; Length 390;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
Matches 87; Conservative 55; Mismatches 126; Indels 116; Gaps 18;

Qy 7 LNAAPKONTWYAGKGL-----CWSQYHDTGYGNGFQNNNGPTRNDQLCA- 51
Db 16 LNSAQENTVPATGQLPAKVAFARNKAGSNWFTVLOGGVAAQFLNDDNNKDLMDRLGAI 75
Qy 52 -----GAFGGYQVNPYLG---FEMGYD----- 70
Db 76 GSLSVGKYHSPFPATRLQINGQQAHTFLGNGEQEINTNFGAAHFDPMFVNVYFAPYRE 135
Qy 71 -----WLGRLMAYKGSVNGAFKAQGVQ-LTKLGLGYPTDDLDIYTRLGGVY-WRAD 120
Db 136 NRFFPHLIPWVG-VGYQHKFIGSEWSKDNVESLTANVGWMA-----FRLGKRVDFVIEA 188
Qy 121 KGNVASTGVSRSSEHDTGVSVPF---AG---GVEWAVTRDIATRL-----EYQWV 163
Db 189 QAAHSNLSRA-YNAKKTVPFEDPAGRYNGFGCMATAGLNFRLGAVGFNAIPMDVALI 247
Qy 164 NNIGDAGTVGTRPDNGMLSLGVSYRFQGE---DAAPVWAP-APAPAPEVATKHFTLKSD 218
Db 248 NDL-----NGQIN-----RLRSEVELSKRPVSCPECEPVPVTKTENILTEKA 291
Qy 219 VLFNFKATLKPEQQALDQLYTQLSNMDPKGSAAVLGYTDRIGSEAYNQQLSEKRAQ 278
Db 292 VLFRFDSHWV---DKDQLINLYDVAQFVKETNEPIVTVGVADPTGNTQYNEKLSERRAKA 348
Qy 279 VVDYLVAK-GIPACKISARGMGES 301
Db 349 VVDVLTGRYGVPSBELISVEWKGDS 372

RESULT 53
US-10-122A-69451
; Sequence 69451, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 69451
LENGTH: 229
TYPE: PRT
ORGANISM: Pseudomonas syringae
US-10-282-122A-69451

Query Match 9.6%; Score 174.5; DB 15; Length 229;
Best Local Similarity 26.8%; Pred. No. 1.2e-07;
Matches 59; Conservative 34; Mismatches 98; Indels 29; Gaps 7;
QY 119 DSKGNVYAGTGVSRSEHDTGVSPVFAAGVWAVTRDIATRLVYQWVNNIGDAGTVGTRPDN 178
DB 27 DNQQAQSGGSKTAKYGGGLAGAVAGAA-----IDH---NNRGKALIGAAV-A 75
QY 179 GMLSLGVSYRFGQDAAPVAPAPAPAPVATKHTFLKSDVLNFNFKATLKPEGQALDQ 238
DB 76 GAASAGYGYADKQGA-LRASMANTGVVEVQVQGGQIKLIMPNTFPAT---DSSAIASS 131
QY 239 LYTLQLSNM-----DPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKI 293
DB 132 FYSPLNNLANSCLKFQNNQNIETIGYTDSTGSRQHMDLSQQRAQSVATYLTSGVDQSHL 191
QY 294 SARGMGSENPVTGTCNDVNKAPAAALICLAPDRRVEIEVK 333
DB 192 SVRGAGPQPTASNADANGRAQ-----NRRVEVNLK 222

RESULT 54
US-10-323-069A-123
Sequence 123, Application US/10323069A
Publication No. US2003028328A1
GENERAL INFORMATION:
APPLICANT: Hardham, John M.
APPLICANT: King, Kendall W.
TITLE OF INVENTION: VACCINE FOR PERIODONTAL DISEASE
FILE REFERENCE: PC11864A

CURRENT APPLICATION NUMBER: US/10/323,069A
CURRENT FILING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 123
LENGTH: 375
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: P. gulae B69
OTHER INFORMATION: OprF polypeptide sequence
US-10-323-069A-123

Query Match 9.3%; Score 169.5; DB 15; Length 375;
Best Local Similarity 23.2%; Pred. No. 6.9e-07;
Matches 78; Conservative 53; Mismatches 117; Indels 88; Gaps 16;
QY 18 AGGKLGSQYHDTGFGNGFQNNNGPTR-----NDQLGA-----GATGG 56
DB 66 ATGSISVGKYHNP-FFATRLQINGGQAHFTFLGKNAEQEINTNFGAAHDFMFDVVVYFAP 124
QY 57 YQVN-----PYLGFEMGYDMLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDDLDIVTR 110
DB 125 YRENRFPHLPWVGVGQHKFISEWSKDNVES-----LTANMGVMA-----FR 169
QY 111 LGGMV-WRADSKGNVYASTGVSRSEHDTGVSPV-----AGGVEWAVTRDIATRL----- 158
DB 170 LGRVDFVIEAQAHAHNLNLSRA-FNAKKTPIFDHQEGRYNGFGMATAGLNFRLGAVG 228
QY 159 -----EYQWVNNIGDAGTVGTRPDNGLSLGVSYPGQE-----DAAPVAP-APAPAP 206
DB 229 FNATPEMDYALINDL-----NGQIN-----RLRREVEBELSKRPVSCPCPDVTP 272
QY 207 EVATKHTFLKSDVLNFNFKATLKPEGQALDQVLTQLSNMDPKDGSVAVLVGYTORIGSEA 266
DB 273 VTKENKLEKAVLFRFDSYV---DKQLNLINDVAGFVKETNEPITVVGADPTGSTQ 329
QY 267 YNOOLSEKRAQSVVDYLVAK-GIPAGKISARGMGES 301
DB 330 YNERLSERRAKAVVDVLTKGYVPSSELISVEWKGDS 365

RESULT 55
US-10-851-965-123
Sequence 123, Application US/10851965
Publication No. US20050010032A1
GENERAL INFORMATION:
APPLICANT: Hardham, John M.
APPLICANT: King, Kendall W.
TITLE OF INVENTION: VACCINE FOR PERIODONTAL DISEASE
FILE REFERENCE: PC11864A
CURRENT APPLICATION NUMBER: US/10/851,965
CURRENT FILING DATE: 2004-05-21
PRIOR APPLICATION NUMBER: US/10/323,069
PRIOR FILING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 123
LENGTH: 375
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: P. gulae B69
OTHER INFORMATION: OprF polypeptide sequence
US-10-851-965-123

Query Match 9.3%; Score 169.5; DB 17; Length 375;
Best Local Similarity 23.2%; Pred. No. 6.9e-07;
Matches 78; Conservative 53; Mismatches 117; Indels 88; Gaps 16;
QY 18 AGGKLGSQYHDTGFGNGFQNNNGPTR-----NDQLGA-----GATGG 56
DB 66 ATGSISVGKYHNP-FFATRLQINGGQAHFTFLGKNAEQEINTNFGAAHDFMFDVVVYFAP 124


```
Qy 71 -----WLGKMGKSGVNDGAFKAGQVQ-LTAKLGYPIITDDLDIYTRLGGMV-WRADS 120
Db 128 NRFFHLIPWVG-VGYQHKFISGSKSKONVELSANLGVMMMA-----FRLGKRVDFVIEA 180
Qy 121 KGNVASTGVRSEHDTGVSFVFA-----GGVEMAVTRDIATRL-----EYQW 162
Db 191 QAAHSNLSRA-FNAKFTPIFQDEGRYNGFGQMATAGLFRLGAVGFNAIEPMDYAL 239
Qy 163 VNNIGDAGTVTRPDNGMLSGVSRFQGE-----DAAPVAP-APAPAPEVATKHTFLKS 217
Db 240 INDL-----NGQIN-----RLRREVEELSRRVSCPECPDVTPTKTENKLTKEK 283
Qy 218 DVLNFKNATLKPEQQALDOLYTQLSNMDPKDGSVAVLGYTDRLGSEAYNQOLSEKRAQ 277
Db 284 AVLFRFDSYVV---DKOQLINLYDVAQVKTNEPTVVGADPTGDTQYNERLSERRAK 340
Qy 278 SVVDYLVAK-GIPAGKISARGMGES 301
Db 341 AVVDVLTGKYVPSSELSVENVKGD 365

RESULT 62
US-10-467-421-39
; Sequence 39, Application US/10467421
; Publication No. US20040116665A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Denoel, Philippe
; APPLICANT: Neyt, Cecile Anne
; APPLICANT: Poolman, Jan
; APPLICANT: Thonnard, Joelle
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45259
; CURRENT APPLICATION NUMBER: US/10/467,421
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/EP02/01361
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103171.5
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 453
; TYPE: PR1
; ORGANISM: Moraxella catarrhalis
US-10-467-421-39

Query Match 9.1%; Score 165.5; DB 16; Length 453;
Best Local Similarity 21.1%; Pred. No. 2.1e-06;
Matches 83; Conservative 50; Mismatches 143; Indels 117; Gaps 13;

Qy 40 NNGPTRNDQLGAGAGGYQVNPYLGFMGYDNLGMRMAYKGSVDNGAFKAGQVQLTAKL-- 97
Db 69 NGGVALDSELTWGAAGIIELTPTQFQVEYGIENRDAKSSDKSAHRFPDABQETISGNFLI 128
Qy 98 -----GYPITDLDLIYTRLG-----GMWRADSKGNVASTGVRSEHDTGVS 139
Db 129 GTEQPSGYNPTNKKFKPYVLVAGQOSKIKVNAIDGYTAEVANGONIAKQVAKGQVAES 188
Qy 140 PVFAG-----GVEMAVTRDIATRLGYQVNNIGDAGTVGTRPDN---GMLSIGVSYRFG- 190
Db 189 KDTIGNLGLGARYLUNDALALRGARATHNF-----DNKWEGLALAGLEVTLGG 238
Qy 191 -----QEDAAPVAPAPA-----PAPE-----VATKHTFLKSD----- 218
Db 239 RLAPAVPVAPAEVAPAEVAPVAPVILKPEPEPEVIEBAPAVIEDIVVDSGDGDPDHL 296
Qy 219 -----VLFNFKNATLKPEQQALDOLYTQLSNMD 247
Db 299 ACPGTPVNTVDPGCPQVNVNLELRLQELRVFFDYDKSIKPKQYREEVAKVAAQMBEF- 357
Qy 248 PKDGSVAVLGYTDR---IGSEAYNQOLSEKRAQSVVDYLVAK-GIPAGKISARGMGESNP 303
```

```
Db 358 -PNATATIEGHASRDSARSARYNQRLSERANAVKSMLSNEFGIAENRLNAVGVGFD 416
Qy 304 VTGNVTGNVKARAALDCLAPDRRVEIEVKGK 336
Db 417 IAPNTTAEGKAM-----NRRVEAVITGSK 440

RESULT 63
US-10-335-977-5248
; Sequence 5248, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
ADDRESSSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 5248:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...179
SEQUENCE DESCRIPTION: SEQ ID NO: 5248:
US-10-335-977-5248

Query Match 8.9%; Score 162.5; DB 15; Length 179;
Best Local Similarity 29.5%; Pred. No. 1.1e-06;
Matches 49; Conservative 25; Mismatches 73; Indels 19; Gaps 4;

Qy 169 AGTGTGTRPDNGMLSLGVSRYRFGQEDAAPVAVAPAPAPAEVATKHTFLKSDVLFNFKATL 228
Db 29 AGDVSTK---AVQTAPVTTPAPEKEEPKPEPAPVVEKPAIESGTIIASIFYDFDKTEI 85
Qy 229 KPEQQALDOLYTQLSNMDPKDGSVAVL---GYTDRIGSEAYNQOLSEKRAQSVVDYLVAK 286
Db 86 KESDQETLDEIVQK-----AKENHMQLLEGNTDFGSGSEYNOALGVKRTLSVKNALVIK 140
Qy 287 GIPAGKISARGMGESNPVTGNVTGNVKARAALDCLAPDRRVEIEV 332
Db 141 GVEKDMIKTISFGESKP-----KCVQKTRCYRENRRVDVKL 177
```

RESULT 64

```

US-10-335-977-5249
; Sequence 5249, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
;

```

NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

```
?  
?  
? COMPUTER READABLE FORM:  
?  
? MEDIUM TYPE: CD-ROM ISO9660  
?  
? COMPUTER: IBM PC Compatible  
?  
? OPERATING SYSTEM: Windows NT 4.0  
?  
? SOFTWARE: UNIX
```

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/ DOI DRAW: 081X
/
/ CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/10/335,977
/   FILING DATE: 30-Dec-2002
/
/ PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: 08/993,002
/   FILING DATE: 17-DEC-1997
/

```

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400

TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 5249:
SEQUENCE CHARACTERISTICS:

```

LENGTH: 179 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori

```

```

/ ORIGIN: HELICOPTER PLANT
/
/ FEATURE:
/
/ NAME/KEY: misc_feature
/ LOCATION: (B) LOCATION 1...179
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 5249:
US-10-335-977-5249

```

Query Match	8.9%	Score 162.5;	DB 15;	Length 179
Best Local Similarity	29.5%	Pred. No. 1.1e-06;		

Matches	49;	Conservative	25;	Mismatches	73;	Indels	19
Qy	169	AGTGTGTRPDNGMLSLGYSYR	FCQEDAA	PVVA	PAPAPAPAPAVATKHFLKSDVL		
		:	:	:	:	:	:
		:	:	:	:	:	:
Db	29	AGDVSTK	--A	VQTAPVTTEPAPEKEE	KQEPAPVVEKPAISGTTI	IASIYI	
		:	:	:	:	:	:
		:	:	:	:	:	:
Qy	229	KPEGQALDQLYTQLSNM	DPKGS	AVL	--GYTDRIGSEAYNQOLSEKRAQS		
		:	:	:	:	:	:
		:	:	:	:	:	:
Db	86	KESDQETLDEIVQK	----	AKENHMOVLLEGN	TDFSGSEYNQALGVKRTLS		
		:	:	:	:	:	:
		:	:	:	:	:	:

[illegible]

US-10-333-977-5250
; Sequence 5250, Application US/10335977
; Publication No. US20040052799A1

IDENTIFICATION NO.: 00000000000000000000

GENERAL INFORMATION:
 APPLICANT: DOUGLAS SMITH et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
 RELATING TO HELICOBACTER PYLORI FOR
 DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

ZIR: 021090103
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX

SOFTWARE: UNLX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/993, 002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36 207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 5250:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid

TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: *Helicobacter pylori*

FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...187
SEQUENCE DESCRIPTION: SEQ ID NO: 5250:
0-335-977-5250

Best Local Similarity 21.7%, Pred. No. 4.6e-05;
Matches 71; Conservative 52; Mismatches 128; Indels 76; Gaps 14;

Qy 26 QYHDTGTGNGFGQNNGPT-----RNDQLCAGA-----FCGY----- 57
 :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 72 KWHNP-YFATELQVFGGPTTFYKNAAGKVOMKENAMAGAHDFMFEDVVNYFKYNPKRV 130
 :|: :|: :|: :|: :|: :|: :|: :|: :|:
Qy 58 -QVNPLYLGFEMGVDMWLRMA-----YKGSVDNAGFAKAGVOLTKAKLGVPITDDL 105
 :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 131 FHLVPWFVGVGYPKTHNDFAEMSDIIKFNEPYRHSAATANAGLMWSFLAKRLDL-VLEGQ 189
 :|: :|: :|: :|: :|: :|: :|: :|: :|:
Qy 106 DIVTRLGGVMWRADSKGNVASTGVSRSSEHTGVSPPVAGGVENAVTR--DIATRLEYOW 162
 :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 190 AIVSLNIVKQEID----YKAPTPYSPTYNLGLGVVTAGLNFNGLRGVAWETVTPMDMDL 245
 :|: :|: :|: :|: :|: :|: :|: :|: :|:
Qy 163 VNNIGDAGTVGTRPDNGMLSLGVSYRFGQDAAPVWPAPAP-APEVATKHFTLKSDVL- 220
 :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 246 INDL-----NQIN-----RLRSENTELKRFPVSCPCEPVSKETTIVVTENVLG 289
 :|: :|: :|: :|: :|: :|: :|: :|: :|:
Qy 221 -----FNFNKATLKPEGOQQALDQLYTOLSNMDFKDSAVVLGYTDRTIGSEAYNQQLSEKR 275
 :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 290 DKAIVKFNFSATTISKDHIVLQDIADFVKI---GNKGVAVIGFADVTDGDANYNMQLSERR 346
 :|: :|: :|: :|: :|: :|: :|: :|: :|:
Qy 276 AQSVVDYLVAK-GIPACKISARGMGES 301
 :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 347 AKAAEALVNQFVPSDMIWEVWQGET 373
 :|: :|: :|: :|: :|: :|: :|: :|: :|:

RESULT 78
US-10-238-075-784
; Sequence 784, Application US/10238075
; Publication No. US20030148324A1
; GENERAL INFORMATION:
; APPLICANT: I.N.S.E.R.M.
; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolated from Escherichia coli
; FILE REFERENCE: BLANDINE
; CURRENT APPLICATION NUMBER: US/10/238,075
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 0003145
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 784
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-238-075-784

```

? Publication No. US20030228328A1
?
? GENERAL INFORMATION:
?
? APPLICANT: Hardham, John M.
? APPLICANT: King, Kendall W.
?
? TITLE OF INVENTION: VACCINE FOR PERIODONTAL DISEASE
?
? FILE REFERENCE: PC11964A
?
? CURRENT APPLICATION NUMBER: US/10/323,069A
?
? CURRENT FILING DATE: 2002-12-18
?
? NUMBER OF SEQ ID NOS: 137
?
? SOFTWARE: PatentIn Ver. 2.1
?
? SEQ ID NO 122
?
? LENGTH: 382
?
? TYPE: PRT
?
? ORGANISM: Artificial Sequence
?
? FEATURE:
?
? OTHER INFORMATION: Description of Artificial Sequence:P.
?
? OTHER INFORMATION: circumdentaria B52 OprF polypeptide sequence
?
? US-10-323-069A-122

```

```

RESULT 80
US-10-851-965-122
; Sequence 122, Application US/10851965
; Publication No. US20050010032A1
; GENERAL INFORMATION:
; APPLICANT: Hardham, John M.
; APPLICANT: King, Kendall W.
; TITLE OF INVENTION: VACCINE FOR PERIODONTAL DISEASE
; FILE REFERENCE: PC11864A
; CURRENT APPLICATION NUMBER: US/10/851,965
; CURRENT FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: US/10/323,069
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:P.
; OTHER INFORMATION: circumdentaria B52 Oprf polypeptide sequence
US-10-851-965-122

```

RESULT 79
US-10-323-069A-122
: Sequence 132. Application US/10323069A


```
; PRIOR APPLICATION NUMBER: PCT/AU01/00482
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: AU PQ 7182
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-283-024-4

Query Match          7.3%; Score 133; DB 15; Length 380;
Best Local Similarity 24.3%; Pred. No. 0.0018;
Matches 77; Conservative 44; Mismatches 130; Indels 66; Gaps 18;

Qy 17 YAGKGLGWSQYHDTGFYGNFGQNNNGPTRNDQLG-----AGAFGGYQVN-----PYLGF 65
Db 85 YFGTRLQFTGDIYGFPGQSKERNHNYFGNAHLDFMFDLTNYFGYRNRVFIHPWAGI 144

Qy 66 EMGYDWLGRMA---YKGSVDN--GAFKAQGVOLTAKLGYPTDLDLDIYTRLGGMVWRADS 120
Db 145 GFYKFXHSENGEKGKDDMTGTNNV-GMLKFLRLSRVVDVFNIEGQAFAGKM-----197

Qy 121 KGNVASTGVSRSSEHDTGVSVPFA-----GGVEWAVTRDIATRLRYOWNNIGDAGTV 172
Db 198 --NF--IGTKRGKAD---FPWATAGLTNFKGTEWTE-----IVPMDYALVNDL-----240

Qy 173 GTRPDNGMLSLGVSRYFQED---AAPVAP-APAPAEVATKHFTLKSDVLFNFKATL 228
Db 241 ----NNQINSLR-----QVSELSRRPVSCEPCEPTQPTVTR-VVDNVVYFRINSA--288

Qy 229 KPEGQALDQLYTQLSNMMDPKGSNAVVLGYTD-RIGSEAYNQOLSEKRAQSVVDYLVAKG 287
Db 289 KIDRNOEIN-VYNTAEYAKTNNAPIKVVGIADEKGTGTAAYNMKLSERRAKAVAKMLEKYG 347

Qy 288 IPAGKISARGMGESNPV 304
Db 348 VSADRIITIEWKGSSEQI 364
```

```
RESULT 88
US-09-998-279-24
; Sequence 24, Application US/09998279
; Publication No. US20030083287A1
; GENERAL INFORMATION:
; APPLICANT: BURGESS, NICOLA A.
; APPLICANT: GARCIA, MIGUEL M.
; APPLICANT: KIRKE, DAVID F.
; APPLICANT: MEYERS, NICHOLAS L.
; APPLICANT: WILLIAMS, PAUL
; TITLE OF INVENTION: Gins
; FILE REFERENCE: GMS0081
; CURRENT APPLICATION NUMBER: US/09/998,279
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/250,288
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-998-279-24

Query Match          7.3%; Score 133; DB 10; Length 385;
Best Local Similarity 24.3%; Pred. No. 0.0018;
Matches 77; Conservative 44; Mismatches 130; Indels 66; Gaps 18;

Qy 17 YAGKGLGWSQYHDTGFYGNFGQNNNGPTRNDQLG-----AGAFGGYQVN-----PYLGF 65
Db 90 YFGTRLQFTGDIYGFPGQSKERNHNYFGNAHLDFMFDLTNYFGYRNRVFIHPWAGI 149
```

```
Qy 66 EMGYDWLGRMA---YKGSVDN--GAFKAQGVOLTAKLGYPTDLDLDIYTRLGGMVWRADS 120
Db 150 GFYKFXHSENGEKGKDDMTGTNNV-GMLKFLRLSRVVDVFNIEGQAFAGKM-----202

Qy 121 KGNVASTGVSRSSEHDTGVSVPFA-----GGVEWAVTRDIATRLRYOWNNIGDAGTV 172
Db 203 --NF--IGTKRGKAD---FPWATAGLTNFKGTEWTE---IVPMDYALVNDL-----245

Qy 173 GTRPDNGMLSLGVSRYFQED---AAPVAP-APAPAEVATKHFTLKSDVLFNFKATL 228
Db 246 ----NNQINSLR-----QVSELSRRPVSCEPCEPTQPTVTR-VVDNVVYFRINSA--293

Qy 229 KPEGQALDQLYTQLSNMMDPKGSNAVVLGYTD-RIGSEAYNQOLSEKRAQSVVDYLVAKG 287
Db 294 KIDRNOEIN-VYNTAEYAKTNNAPIKVVGIADEKGTGTAAYNMKLSERRAKAVAKMLEKYG 352

Qy 288 IPAGKISARGMGESNPV 304
Db 353 VSADRIITIEWKGSSEQI 369

RESULT 89
US-10-450-763-48136
; Sequence 48136, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 48136
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (241)..(277)
; OTHER INFORMATION: OmpA-like domain proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL01068, p-value=7.188e-13, raw score of 21.59
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (210)..(306)
; OTHER INFORMATION: OmpA family domain identified by Pfam, accession name OmpA, E
; OTHER INFORMATION: -value=1.9e-43, Pfam score of 157.7
US-10-450-763-48136

Query Match          7.2%; Score 130.5; DB 18; Length 315;
Best Local Similarity 28.7%; Pred. No. 0.0023;
Matches 39; Conservative 20; Mismatches 44; Indels 33; Gaps 5;

Qy 215 LKSDVLFNFKATLKPEGQALDQLYTQLSN-----MDPKGSNAVVLGYTDRISEAY 267
Db 205 LSDAILFAKNDYKLLPESQQIQITMAAKLASTGLTHARM-----GHTDNYGEDSY 255

Qy 268 NQQLSEKRAQSVVDYLVAKG-IPAGKISARGMGESNPVTGNTCNVVARAALIDCLAPDR 326
Db 256 NEGLSLKRANVADAWAMGGQIPRSNLTTOGLGKKYPIASNKTAQGRAB-----NR 306

Qy 327 RVELEVKGXEVVTPQ 342
Db 307 RVAV-----VIITP 315

RESULT 90
```

```
US-10-323-069A-125
; Sequence 125, Application US/10323069A
; Publication No. US2003028328A1
; GENERAL INFORMATION:
; APPLICANT: Hardham, John M.
; TITLE OF INVENTION: VACCINE FOR PERIODONTAL DISEASE
; FILE REFERENCE: PC11864A
; CURRENT APPLICATION NUMBER: US/10/323,069A
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 316
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P.
; OTHER INFORMATION: canggingivalis B98 OprF polypeptide sequence
US-10-323-069A-125

Query Match          7.1%; Score 128.5; DB 15; Length 316;
Best Local Similarity 21.0%; Pred. No. 0.0036;
Matches 65; Conservative 48; Mismatches 121; Indels 75; Gaps 13;

QY 26 QYHDTGFYNGFQNNNGPT-----RNDQLGAGA-----FGGY----- 57
DB 30 KWHNP-YFATRLQVFGGPTPTFYKNAAGVKMENAAMAGAHDFDMFVNVYFGKYNPKRV 88
QY 58 -QVNPYLGFEMGYDMLGRMA-----YKGSVDNGAFKAQGVQVLTAKLGYPTITDDL 105
DB 89 FHLVPFWGVGYGFKYHNDFAEMSDIIKFNPEYRHSATANAGLMMSFRLAKRLDL-VLSE 147
QY 106 DIYTRLGMMWRADSKGNVASTGVSRSRSHDTGVSVPFAGGVWAVTR---DIATRL 162
DB 148 AIYSNLNIVKQID----YKAPSTPSPYNGLLGVVTTAGLNFNLGRVAVETVTPMDMDL 203
QY 163 VNNIGDAGTVGTRPDNGMLSLGVSVYRFGQDAAPVAPAPAP-APAVATKHTLKS 220
DB 204 INDL-----NGQIN-----RLRSENTELKRPVSCPEVSKETTVVTENVLG 247
QY 221 -----FNFNKATLKPEGQOALDQLYTQLSNMDPKDGSVAVLGYTDRIGSEAYNOOLSEKR 275
DB 248 DKAIVFKFNSATISKDQHIVLQDIADFKVN---GNKGVAVIGFADVTGDANYNMQLSERR 304
QY 276 AQSVDVYLV 284
DB 305 AKAVAEALV 313

RESULT 91
US-10-323-069A-125
; Sequence 125, Application US/10851965
; Publication No. US20050010032A1
; GENERAL INFORMATION:
; APPLICANT: Hardham, John M.
; TITLE OF INVENTION: VACCINE FOR PERIODONTAL DISEASE
; FILE REFERENCE: PC11864A
; CURRENT APPLICATION NUMBER: US/10/851,965
; PRIOR FILING DATE: 2004-05-21
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 316
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P.
; OTHER INFORMATION: canggingivalis B98 OprF polypeptide sequence
US-10-851-965-125

Query Match          7.1%; Score 128.5; DB 15; Length 316;
Best Local Similarity 21.0%; Pred. No. 0.0036;
Matches 65; Conservative 48; Mismatches 121; Indels 75; Gaps 13;

QY 26 QYHDTGFYNGFQNNNGPT-----RNDQLGAGA-----FGGY----- 57
DB 30 KWHNP-YFATRLQVFGGPTPTFYKNAAGVKMENAAMAGAHDFDMFVNVYFGKYNPKRV 88
QY 58 -QVNPYLGFEMGYDMLGRMA-----YKGSVDNGAFKAQGVQVLTAKLGYPTITDDL 105
DB 89 FHLVPFWGVGYGFKYHNDFAEMSDIIKFNPEYRHSATANAGLMMSFRLAKRLDL-VLSE 147
QY 106 DIYTRLGMMWRADSKGNVASTGVSRSRSHDTGVSVPFAGGVWAVTR---DIATRL 162
DB 148 AIYSNLNIVKQID----YKAPSTPSPYNGLLGVVTTAGLNFNLGRVAVETVTPMDMDL 203
QY 163 VNNIGDAGTVGTRPDNGMLSLGVSVYRFGQDAAPVAPAPAP-APAVATKHTLKS 220
DB 204 INDL-----NGQIN-----RLRSENTELKRPVSCPEVSKETTVVTENVLG 247
QY 221 -----FNFNKATLKPEGQOALDQLYTQLSNMDPKDGSVAVLGYTDRIGSEAYNOOLSEKR 275
DB 248 DKAIVFKFNSATISKDQHIVLQDIADFKVN---GNKGVAVIGFADVTGDANYNMQLSERR 304
QY 276 AQSVDVYLV 284
DB 305 AKAVAEALV 313

RESULT 92
US-10-323-069A-126
; Sequence 126, Application US/10323069A
; Publication No. US2003028328A1
; GENERAL INFORMATION:
; APPLICANT: Hardham, John M.
; TITLE OF INVENTION: VACCINE FOR PERIODONTAL DISEASE
; FILE REFERENCE: PC11864A
; CURRENT APPLICATION NUMBER: US/10/323,069A
; CURRENT FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
; LENGTH: 323
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P. salivosa
; OTHER INFORMATION: B104 OprF polypeptide sequence
US-10-323-069A-126

Query Match          7.0%; Score 127.5; DB 15; Length 323;
Best Local Similarity 21.0%; Pred. No. 0.0046;
Matches 65; Conservative 48; Mismatches 121; Indels 75; Gaps 13;

QY 26 QYHDTGFYNGFQNNNGPT-----RNDQLGAGA-----FGGY----- 57
DB 37 KWHNP-YFATRLQVFGGPTPTFYKNAAGVKMENAAMAGAHDFDMFVNVYFGKYNPKRV 95
QY 58 -QVNPYLGFEMGYDMLGRMA-----YKGSVDNGAFKAQGVQVLTAKLGYPTITDDL 105
DB 96 FHLVPFWGVGYGFKYHNDFAEMSDIIKFNPEYRHSATANAGLMMSFRLAKRLDL-VLSE 154
QY 106 DIYTRLGMMWRADSKGNVASTGVSRSRSHDTGVSVPFAGGVWAVTR---DIATRL 162
DB 155 AIYSNLNIVKQID----YKAPSTPSPYNGLLGVVTTAGLNFNLGRVAVETVTPMDMDL 210
QY 163 VNNIGDAGTVGTRPDNGMLSLGVSVYRFGQDAAPVAPAPAP-APAVATKHTLKS 220
DB 211 INDL-----NGQIN-----RLRSENTELKRPVSCPEVSKETTVVTENVLG 254
QY 221 -----FNFNKATLKPEGQOALDQLYTQLSNMDPKDGSVAVLGYTDRIGSEAYNOOLSEKR 275
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Db      255 DKAIVFKENSATISKDQHIVLQDIADFVKN---GNKGVAVIGFADVTGTDANYNQLSERR 311
      ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      276 AQSVDVYLV 284
      ||:| :| :|
Db      312 AKAVAEALV 320
      ||:| :| :|

RESULT 93
US-10-965-126
; Sequence 126, Application US/10851965
; Publication No. US2005010032A1
; GENERAL INFORMATION:
; APPLICANT: Hardham, John M.
; APPLICANT: King, Kendall W.
; TITLE OF INVENTION: VACCINE FOR PERIODONTAL DISEASE
; FILE REFERENCE: PC11864A
; CURRENT APPLICATION NUMBER: US/10/851,965
; CURRENT FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: US/10/323,069
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:P. salivosa
; OTHER INFORMATION: B104 OprF polypeptide sequence
US-10-851-965-126

Query Match          7.0%; Score 127.5; DB 17; Length 323;
Best Local Similarity 21.0%; Pred. No. 0.0046;
Matches 65; Conservative 48; Mismatches 121; Indels 75; Gaps 13;

Qy      26 QVHDTGFYGNCFQNNNGPT-----RNDQLGAGA-----FGGY----- 57
      :|:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      37 KWHNP-YFATRLQVFGGTFPFYKNAAGVKVKNAMAGAHFDFMFDVVNYFGKYNKRV 95
      :|:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Qy      58 -QVNPYLGFEMGYDWLGRMA-----YKGSVDNGAFKAQGVQLTAKLGYPIITDDL 105
      :|:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      96 FHLVFWFGVGYGKYHNDPFAEWSDIKKNPEYRHSATANAGLMSFRLAKRLDL-VLEGQ 154
      :|:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Qy      106 DIYTRLGWVRADSKGNVASTGVSREHDTGCVSPVFAGGVWAVTR---DIATRLFYQW 162
      ||:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      155 AYSNLNIVKQEID----YKAPSTPSPNYNGLLGVTAGLNFNLGRVAVETIITPMDMDL 210
      :|:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Qy      163 VNNIGDAGTVGTRPDNGMLSLGVSYRFQGEDAAPVVAAPAP-APEVATKHTLTKSDVL- 220
      :|:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      211 INDL-----NGQIN-----RLRSENTELKRPVSCPCEPEVSKETTVVTENVLG 254
      :|:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Qy      221 -----FNFNKATLKPEGOQALDQLYQLSNMDDPKDGSAAVLGYTDRIGSEAYNQOLSEKR 275
      ||:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      255 DKAIVFKENSATISKDQHIVLQDIADFVKN---GNKGVAVIGFADVTGTDANYNQLSERR 311
      ||:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Qy      276 AQSVDVYLV 284
      ||:| :| :|
Db      312 AKAVAEALV 320
      ||:| :| :|

RESULT 94
US-10-920-244A-11
; Sequence 11, Application US/10920244A
; Publication No. US20050196406A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of California
; APPLICANT: DAUGHERTY, Patrick S.
; APPLICANT: BESSETTE, Paul H.
; APPLICANT: RICE, Jeffrey
; TITLE OF INVENTION: Polypeptide Display Libraries and Methods of Making and Using
; FILE REFERENCE: 034044.034

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; CURRENT APPLICATION NUMBER: US/10/920,244A
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: US 60/495,698
; PRIOR FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Enterobacter aerogenes
US-10-920-244A-11

Query Match          6.9%; Score 126.5; DB 18; Length 33;
Best Local Similarity 72.7%; Pred. No. 0.00022;
Matches 24; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy      21 KLGSQVHDTGFYGNCFQNNNGPTRNDQLGAGA 53
      |||||:||||:| ||||| |||||
Db      2 KLGSQFHDGTGWY-NSNLNNGPTHESQLGAGA 33
      |||||:||||:| ||||| |||||

RESULT 95
US-10-920-244A-4
; Sequence 4, Application US/10920244A
; Publication No. US20050196406A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of California
; APPLICANT: DAUGHERTY, Patrick S.
; APPLICANT: BESSETTE, Paul H.
; APPLICANT: RICE, Jeffrey
; TITLE OF INVENTION: Polypeptide Display Libraries and Methods of Making and Using
; FILE REFERENCE: 034044.034
; CURRENT APPLICATION NUMBER: US/10/920,244A
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: US 60/495,698
; PRIOR FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-920-244A-4

Query Match          6.9%; Score 125.5; DB 18; Length 29;
Best Local Similarity 72.7%; Pred. No. 0.00023;
Matches 24; Conservative 1; Mismatches 3; Indels 5; Gaps 1;

Qy      21 KLGSQVHDTGFYGNCFQNNNGPTRNDQLGAGA 53
      |||||:||||| |||||:|||||
Db      2 KLGSQVHDTGFI-----NNNGPTHESQLGAGA 29
      |||||:||||| |||||:|||||

RESULT 96
US-10-920-244A-6
; Sequence 6, Application US/10920244A
; Publication No. US20050196406A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of California
; APPLICANT: DAUGHERTY, Patrick S.
; APPLICANT: BESSETTE, Paul H.
; APPLICANT: RICE, Jeffrey
; TITLE OF INVENTION: Polypeptide Display Libraries and Methods of Making and Using
; FILE REFERENCE: 034044.034
; CURRENT APPLICATION NUMBER: US/10/920,244A
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: US 60/495,698
; PRIOR FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6

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Db	243	TDFTQILSHAV	6.9%; Score 125.5; DB 18; Length 29; Best Local Similarity 72.7%; Pred. No. 0.0023; Matches 24; Conservative 1; Mismatches 3; Indels 5; Gaps 1;	
Qy	135	-----DTG--VSPVFAGVWEAVT--RDIATRLLEYQWVNNIGDAGTGTGTRPDNGMLSLGVSYSR 188		
Db	295	LYAIDTGLGGMGAKITLSTDRDASVRNGQW---FASAGNVAVNAEGKLVNTGMAA 351		
Qy	189	FGQEDAAPVVPAPAPAPAPAVATK-HFTLKSDVLPFNFKATLKPQEQALDQ-----239		
Db	352	TGENHAVSLHARNVHNSGTVASQDDANIHSQTL--DNSGTVLSSQQLTVRNLRGLKNHNN 409		
Qy	240	-YTQLSNMDPKDGSNAVVLGYTDTRIGSEAYN-----QQLSEKRAQSUV 280		
Db	410	GTIOAARLDMTGGLDNTGNITQTGSQALDLVSAGKFDNSGKIGVSDVPQTGLNPNPSVI 469		
Qy	281	DYL--VAKGIPAGKISARGMESNPVT 305		
Db	470	PQIPSTATGSGSSTVSASKPGSNPNVS 496		
RESULT 98				
US-10-639-387-4				
; Sequence 4, Application US/10639387				
; Publication No. US2005009037A1				
; GENERAL INFORMATION:				
; APPLICANT: Chang, Yung-Fu				
; APPLICANT: Simpson, Kenneth W				
; APPLICANT: Zhu, Jiaqian				
; TITLE OF INVENTION: HELICOBLACTER BIZZOZERONII OUTER MEMBRANE PROTEIN				
; TITLE OF INVENTION: ENCODING GENE AND ITS USE IN DIAGNOSTIC AND TREATMENT				
; TITLE OF INVENTION: METHODS				
; FILE REFERENCE: 19603/4181				
; CURRENT APPLICATION NUMBER: US/10/639,387				
; CURRENT FILING DATE: 2003-08-12				
; PRIOR APPLICATION NUMBER: 60/404,340				
; PRIOR FILING DATE: 2002-08-16				
; NUMBER OF SEQ ID NOS: 9				
; SOFTWARE: PatentIn Ver. 2.1				
; SEQ ID NO 4				
; LENGTH: 168				
; TYPE: PRT				
; ORGANISM: Brucella abortus				
US-10-639-387-4				
Query Match 6.7%; Score 122; DB 17; Length 168;				
Best Local Similarity 23.4%; Pred. No. 0.0059;				
Matches 39; Conservative 26; Mismatches 54; Indels 48; Gaps 7;				
Qy	164	NNIGDAGTVGTRPDNGMLSLGVSYSRFGQEDAAPVVPAPAPAPAPAVATKHFHLK--SDVLF 221		
Db	33	NNAGDLG-----LG-----AGAATFG---SSQDFTVNVGDRIFP 63		
Qy	222	NFNKATLKPEQQAALD-----QYTLQSLNMDPKDGSNAVVLGYTDTRIGSEAYNQQLSEKR 275		
Db	64	DLDSLRIRADAQOTLSKQAQWLQRYQY-----SITIEGHADERGTREYNALGQRR 115		
Qy	276	AGSVVDYLVAKGIPAGKISARGMESNPVT---GNTCDNVKARAALI 319		
Db	116	AAATRDFLASRGVPTNRMTISYGNRNPVAVCDADTCWSONRRRAVTV 162		
RESULT 99				
US-10-323-069A-121				
; Sequence 121, Application US/10323069A				
; Publication No. US2003028328A1				
; GENERAL INFORMATION:				
; APPLICANT: Hardham, John M.				
; APPLICANT: King, Kendall W.				
; TITLE OF INVENTION: VACCINE FOR PERIODONTAL DISEASE				
; FILE REFERENCE: PCI1864A				
; CURRENT APPLICATION NUMBER: US/10/323,069A				
; CURRENT FILING DATE: 2002-12-18				
; NUMBER OF SEQ ID NOS: 137				

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:P. cansulci B46
; OTHER INFORMATION: OprF polypeptide sequence
US-10-323-069A-121

Query Match          6.7%; Score 121.5; DB 15; Length 366;
Best Local Similarity 20.8%; Pred. No. 0.02;
Matches 82; Conservative 43; Mismatches 122; Indels 147; Gaps 21;

Qy  7 LNAAPKNTWTAGCKLHWSQVHDTGF-----YNGFQNNNGPTRNDOLGAGAFG- 55
Db  20 MGQTPAKNTAYARSEAG-----DNWFTVLOGGAAMQFGKG--NEDADFFDRQTVAPTFAV 72
Qy  56 GYQVNPYLG-----FEMGYD----- 70
Db  73 GKWHNPFPGTFLQMLGVSHDFSNNEAKSKLEMHARYANAHFDFMDFVINYFKPYSEDR 132
Qy  71 -----WLGRLMAYKGSVD--NGAFKAQGVQLTAKLG-----YPITDLDLI----- 107
Db  133 VFHLIPWVG--LGYDHKPEKSNFKVDA--LTANAGLMPAFRVMERMDIVLESQVMYSDFN 189
Qy  108 -----YTRLGMMWRADSKGNVASTGVSRSSEHDTGSPVPFAGGVEWAVTRDIATRL 158
Db  190 LNTALPEPRYTACSGML-----TAGLNFRIGNIGWSEILP--MDWGLVNDLNGQI 237
Qy  159 EYQWVNNIGDAGTVGTFRPDNGLSLGVSYSRFGQEDAAPVVP-APAPAPEVATKHFTLKS 217
Db  238 N-----AMRAKNAELS-----KRPVSCPECEPEPRVERINMLSDK 273
Qy  218 DVLNFNFNKATLKPEGQQALDQLYT--QLSNMMDPKDGS AV-VLGYTDRIGSEAYNQQLSEK 274
Db  274 SVLFRAGKTTVDS-----DQWVTIFDVAQFAKKNGTQITVTGYADKKGKE--SDRTSEL 325
Qy  275 RAQSVVDYLVAK-GIPAGKISARGMGESNPVTGN 307
Db  326 RAKAVAKILTDKYGVPSDRISIEWKGVSEQVYDN 359

Search completed: September 20, 2005, 21:52:42
Job time : 178 secs
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RESULT 100
US-10-851-965-121
; Sequence 121, Application US/10851965
; Publication No. US20050010032A1
; GENERAL INFORMATION:
; APPLICANT: Hardham, John M.
; APPLICANT: King, Kendall W.
; TITLE OF INVENTION: VACCINE FOR PERIODONTAL DISEASE
; FILE REFERENCE: PC11864A
; CURRENT APPLICATION NUMBER: US/10/851.965
; CURRENT FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: US/10/323,069
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:P. cansulci B46
; OTHER INFORMATION: OprF polypeptide sequence
US-10-851-965-121

Query Match          6.7%; Score 121.5; DB 17; Length 366;
Best Local Similarity 20.8%; Pred. No. 0.02;
Matches 82; Conservative 43; Mismatches 122; Indels 147; Gaps 21;

Qy  7 LNAAPKNTWTAGCKLHWSQVHDTGF-----YNGFQNNNGPTRNDOLGAGAFG- 55
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